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(57) Abstract

Invertebrate and vertebrate *patched* genes are provided, including the mouse and human *patched* genes, as well as methods for isolation of related genes, where the genes may be of different species or in the same family. Having the ability to regulate the expression of the *patched* gene, allows for the elucidation of embryonic development, cellular regulation associated with signal transduction by the *patched* gene, the identification of agonist and antagonist to signal transduction, identification of ligands for binding to *patched*, isolation of the ligands, and assaying for levels of transcription and expression of the *patched* gene.

PATCHED GENES AND THEIR USE

INTRODUCTION

Technical Field

The field of this invention concerns segment polarity genes and their uses.

Background

Segment polarity genes were discovered in flies as mutations which change the pattern of structures of the body segments. Mutations in the genes cause animals to develop the changed patterns on the surfaces of body segments, the changes affecting the pattern along the head to tail axis. For example, mutations in the gene *patched* cause each body segment to develop without the normal structures in the center of each segment. In their stead is a mirror image of the pattern normally found in the anterior segment. Thus cells in the center of the segment make the wrong structures, and point them in the wrong direction with reference to the over all head-to-tail polarity of the animal. About sixteen genes in the class are known. The encoded proteins include kinases, transcription factors, a cell junction protein, two secreted proteins called wingless (WG) and hedgehog (HH), a single transmembrane protein called *patched* (PTC), and some novel proteins not related to any known protein. All of these proteins are believed to work together in signaling pathways that inform cells about their neighbors in order to set cell fates and polarities.

Many of the segment polarity proteins of *Drosophila* and other invertebrates are closely related to vertebrate proteins, implying that the molecular mechanisms involved are ancient. Among the vertebrate proteins related to the fly genes are En-1 and -2, which act in vertebrate brain development and WNT-1, which is also involved in brain development, but was first found as the oncogene implicated in many cases of mouse breast cancer. In flies, the *patched* gene is transcribed into RNA in a complex and dynamic pattern in embryos, including fine transverse stripes in each body segment primordium. The encoded protein is predicted to contain many transmembrane domains. It has no significant similarity to any other known protein. Other proteins having large numbers of transmembrane domains include a variety of membrane receptors, channels through membranes and transporters through membranes.

The hedgehog (HH) protein of flies has been shown to have at least three vertebrate relatives: *Sonic hedgehog* (*Shh*); *Indian hedgehog*, and *Desert hedgehog*. The *Shh* is expressed in a group of cells at the posterior of each developing limb bud. This is exactly the same group of cells found to have an important role in signaling polarity to the developing limb. The signal appears to be graded, with cells close to the posterior source of the signal forming posterior digits and other limb structures and cells farther from the signal source forming more anterior structures. It has been known for many years that transplantation of the signaling cells, a region of the limb bud known as the "zone of polarizing activity (ZPA)" has dramatic effects on limb patterning. Implanting a second ZPA anterior to the limb bud causes a limb to develop with posterior features replacing the anterior ones (in essence little fingers instead of thumbs). *Shh* has been found to be the long sought ZPA signal. Cultured cells making *Shh* protein (SHH), when implanted into the anterior limb bud region, have the same effect as an implanted ZPA. This establishes that *Shh* is clearly a critical trigger of posterior limb development.

The factor in the ZPA has been thought for some time to be related to another important developmental signal that polarizes the developing spinal cord. The notochord, a rod of mesoderm that runs along the dorsal side of early vertebrate embryos, is a signal source that polarizes the neural tube along the dorsal-ventral axis. The signal causes the part of the neural tube nearest to the notochord to form

floor plate, a morphologically distinct part of the neural tube. The floor plate, in turn, sends out signals to the more dorsal parts of the neural tube to further determine cell fates. The ZPA was reported to have the same signaling effect as the notochord when transplanted to be adjacent to the neural tube, suggesting the ZPA makes the same signal as the notochord. In keeping with this view, *Shh* was found to be produced by notochord cells and floor plate cells. Tests of extra expression of *Shh* in mice led to the finding of extra expression of floor plate genes in cells which would not normally turn them on. Therefore *Shh* appears to be a component of the signal from notochord to floor plate and from floor plate to more dorsal parts of the neural tube. Besides limb and neural tubes, vertebrate hedgehog genes are also expressed in many other tissues including, but not limited to the peripheral nervous system, brain, lung, liver, kidney, tooth primordia, genitalia, and hindgut and foregut endoderm.

PTC has been proposed as a receptor for HH protein based on genetic experiments in flies. A model for the relationship is that PTC acts through a largely unknown pathway to inactivate both its own transcription and the transcription of the *wingless* segment polarity gene. This model proposes that HH protein, secreted from adjacent cells, binds to the PTC receptor, inactivates it, and thereby prevents PTC from turning off its own transcription or that of *wingless*. A number of experiments have shown coordinate events between PTC and HH.

Relevant Literature

Descriptions of *patched*, by itself or its role with *hedgehog* may be found in Hooper and Scott, Cell 59, 751-765 (1989); Nakano et al., Nature, 341, 508-513 (1989) (both of which also describes the sequence for *Drosophila patched*) Simcox et al., Development 107, 715-722 (1989); Hidalgo and Ingham, Development, 110, 291-301 (1990); Phillips et al., Development, 110, 105-114 (1990); Sampedro and Guerrero, Nature 353, 187-190 (1991); Ingham et al., Nature 353, 184-187 (1991); and Taylor et al., Mechanisms of Development 42, 89-96 (1993). Discussions of the role of *hedgehog* include Riddle et al., Cell 75, 1401-1416 (1993); Echelard et al., Cell 75, 1417-1430 (1993); Krauss et al., Cell 75, 1431-1444 (1993); Tabata and Kornberg, Cell 76, 89-102 (1994); Heemskerk & DiNardo, Cell 76, 449-460 (1994); Relink et al., Cell 76, 761-775 (1994); and a short review article by

Ingham, Current Biology 4, 347-350 (1994). The sequence for the Drosophila 5' non-coding region was reported to the GenBank, accession number M28418, referred to in Hooper and Scott (1989), *supra*. See also, Forbes, et al., Development 1993 Supplement 115-124.

SUMMARY OF THE INVENTION

Methods for isolating *patched* genes, particularly mammalian *patched* genes, including the mouse and human *patched* genes, as well as invertebrate *patched* genes and sequences, are provided. The methods include identification of *patched* genes from other species, as well as members of the same family of proteins. The subject genes provide methods for producing the patched protein, where the genes and proteins may be used as probes for research, diagnosis, binding of *hedgehog* protein for its isolation and purification, gene therapy, as well as other utilities.

BRIEF DESCRIPTION OF THE DRAWINGS

Fig. 1 is a graph having a restriction map of about 10kbp of the 5' region upstream from the initiation codon of *Drosophila patched* gene and bar graphs of constructs of truncated portions of the 5' region joined to β-galactosidase, where the constructs are introduced into fly cell lines for the production of embryos. The expression of β-gal in the embryos is indicated in the right-hand table during early and late development of the embryo. The greater the number of +'s, the more intense the staining.

DESCRIPTION OF THE SPECIFIC EMBODIMENTS

Methods are provided for identifying members of the *patched* (*ptc*) gene family from invertebrate and vertebrate, *e.g.* mammalian, species, as well as the entire cDNA sequence of the mouse and human *patched* gene. Also, sequences for invertebrate *patched* genes are provided. The *patched* gene encodes a transmembrane protein having a large number of transmembrane sequences.

In identifying the mouse and human *patched* genes, primers were employed to move through the evolutionary tree from the known *Drosophila ptc* sequence. Two primers are employed from the *Drosophila* sequence with appropriate

restriction enzyme linkers to amplify portions of genomic DNA of a related invertebrate, such as mosquito. The sequences are selected from regions which are not likely to diverge over evolutionary time and are of low degeneracy. Conveniently, the regions are the N-terminal proximal sequence, generally within the first 1.5kb, usually within the first 1kb, of the coding portion of the cDNA, conveniently in the first hydrophilic loop of the protein. Employing the polymerase chain reaction (PCR) with the primers, a band can be obtained from mosquito genomic DNA. The band may then be amplified and used in turn as a probe. One may use this probe to probe a cDNA library from an organism in a different branch of the evolutionary tree, such as a butterfly. By screening the library and identifying sequences which hybridize to the probe, a portion of the butterfly *patched* gene may be obtained. One or more of the resulting clones may then be used to rescreen the library to obtain an extended sequence, up to and including the entire coding region, as well as the non-coding 5'- and 3'-sequences. As appropriate, one may sequence all or a portion of the resulting cDNA coding sequence.

One may then screen a genomic or cDNA library of a species higher in the evolutionary scale with appropriate probes from one or both of the prior sequences. Of particular interest is screening a genomic library, of a distantly related invertebrate, *e.g.* beetle, where one may use a combination of the sequences obtained from the previous two species, in this case, the *Drosophila* and the butterfly. By appropriate techniques, one may identify specific clones which bind to the probes, which may then be screened for cross hybridization with each of the probes individually. The resulting fragments may then be amplified, *e.g.* by subcloning.

By having all or parts of the 4 different *patched* genes, in the presently illustrated example, *Drosophila* (fly), mosquito, butterfly and beetle, one can now compare the *patched* genes for conserved sequences. Cells from an appropriate mammalian limb bud or other cells expressing *patched*, such as notochord, neural tube, gut, lung buds, or other tissue, particularly fetal tissue, may be employed for screening. Alternatively, adult tissue which produces *patched* may be employed for screening. Based on the consensus sequence available from the 4 other species, one

can develop probes where at each site at least 2 of the sequences have the same nucleotide and where the site varies that each species has a unique nucleotide, inosine may be used, which binds to all 4 nucleotides.

Either PCR may be employed using primers or, if desired, a genomic library from an appropriate source may be probed. With PCR, one may use a cDNA library or use reverse transcriptase-PCR (RT-PCR), where mRNA is available from the tissue. Usually, where fetal tissue is employed, one will employ tissue from the first or second trimester, preferably the latter half of the first trimester or the second trimester, depending upon the particular host. The age and source of tissue will depend to a significant degree on the ability to surgically isolate the tissue based on its size, the level of expression of *patched* in the cells of the tissue, the accessibility of the tissue, the number of cells expressing *patched* and the like. The amount of tissue available should be large enough so as to provide for a sufficient amount of mRNA to be usefully transcribed and amplified. With mouse tissue, limb bud of from about 10 to 15 dpc (days post conception) may be employed.

In the primers, the complementary binding sequence will usually be at least 14 nucleotides, preferably at least about 17 nucleotides and usually not more than about 30 nucleotides. The primers may also include a restriction enzyme sequence for isolation and cloning. With RT-PCR, the mRNA may be enriched in accordance with known ways, reverse transcribed, followed by amplification with the appropriate primers. (Procedures employed for molecular cloning may be found in Molecular Cloning: A Laboratory Manual, Sambrook et al., eds., Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1988). Particularly, the primers may conveniently come from the N-terminal proximal sequence or other conserved region, such as those sequences where at least five amino acids are conserved out of eight amino acids in three of the four sequences. This is illustrated by the sequences (SEQ ID NO:11) IITPLDCFWEG, (SEQ ID NO:12) LIVGG, and (SEQ ID NO:13) PFFWEQY. Resulting PCR products of expected size are subcloned and may be sequenced if desired.

The cloned PCR fragment may then be used as a probe to screen a cDNA library of mammalian tissue cells expressing *patched*, where hybridizing clones may be isolated under appropriate conditions of stringency. Again, the cDNA library

should come from tissue which expresses *patched*, which tissue will come within the limitations previously described. Clones which hybridize may be subcloned and rescreened. The hybridizing subclones may then be isolated and sequenced or may be further analyzed by employing RNA blots and *in situ* hybridizations in whole and sectioned embryos. Conveniently, a fragment of from about 0.5 to 1kbp of the N-terminal coding region may be employed for the Northern blot.

The mammalian gene may be sequenced and as described above, conserved regions identified and used as primers for investigating other species. The N-terminal proximal region, the C-terminal region or an intermediate region may be employed for the sequences, where the sequences will be selected having minimum degeneracy and the desired level of conservation over the probe sequence.

The DNA sequence encoding PTC may be cDNA or genomic DNA or fragment thereof, particularly complete exons from the genomic DNA, may be isolated as the sequence substantially free of wild-type sequence from the chromosome, may be a 50 kbp fragment or smaller fragment, may be joined to heterologous or foreign DNA, which may be a single nucleotide, oligonucleotide of up to 50 bp, which may be a restriction site or other identifying DNA for use as a primer, probe or the like, or a nucleic acid of greater than 50 bp, where the nucleic acid may be a portion of a cloning or expression vector, comprise the regulatory regions of an expression cassette, or the like. The DNA may be isolated, purified being substantially free of proteins and other nucleic acids, be in solution, or the like.

The subject gene may be employed for producing all or portions of the *patched* protein. The subject gene or fragment thereof, generally a fragment of at least 12 bp, usually at least 18 bp, may be introduced into an appropriate vector for extrachromosomal maintenance or for integration into the host. Fragments will usually be immediately joined at the 5' and/or 3' terminus to a nucleotide or sequence not found in the natural or wild-type gene, or joined to a label other than a nucleic acid sequence. For expression, an expression cassette may be employed, providing for a transcriptional and translational initiation region, which may be inducible or constitutive, the coding region under the transcriptional control of the transcriptional initiation region, and a transcriptional and translational termination

region. Various transcriptional initiation regions may be employed which are functional in the expression host. The peptide may be expressed in prokaryotes or eukaryotes in accordance with conventional ways, depending upon the purpose for expression. For large production of the protein, a unicellular organism or cells of a higher organism, *e.g.* eukaryotes such as vertebrates, particularly mammals, may be used as the expression host, such as *E. coli*, *B, subtilis*, *S. cerevisiae*, and the like. In many situations, it may be desirable to express the *patched* gene in a mammalian host, whereby the *patched* gene will be transported to the cellular membrane for various studies. The protein has two parts which provide for a total of six transmembrane regions, with a total of six extracellular loops, three for each part. The character of the protein has similarity to a transporter protein. The protein has two conserved glycosylation signal triads.

The subject nucleic acid sequences may be modified for a number of purposes, particularly where they will be used intracellularly, for example, by being joined to a nucleic acid cleaving agent, *e.g.* a chelated metal ion, such as iron or chromium for cleavage of the gene; as an antisense sequence; or the like. Modifications may include replacing oxygen of the phosphate esters with sulfur or nitrogen, replacing the phosphate with phosphoramide, etc.

With the availability of the protein in large amounts by employing an expression host, the protein may be isolated and purified in accordance with conventional ways. A lysate may be prepared of the expression host and the lysate purified using HPLC, exclusion chromatography, gel electrophoresis, affinity chromatography, or other purification technique. The purified protein will generally be at least about 80% pure, preferably at least about 90% pure, and may be up to 100% pure. By pure is intended free of other proteins, as well as cellular debris.

The polypeptide may be used for the production of antibodies, where short fragments provide for antibodies specific for the particular polypeptide, whereas larger fragments or the entire gene allow for the production of antibodies over the surface of the polypeptide or protein, where the protein may be in its natural conformation.

Antibodies may be prepared in accordance with conventional ways, where the expressed polypeptide or protein may be used as an immunogen, by itself or

conjugated to known immunogenic carriers, *e.g.* KLH, pre-S HBsAg, other viral or eukaryotic proteins, or the like. Various adjuvants may be employed, with a series of injections, as appropriate. For monoclonal antibodies, after one or more booster injections, the spleen may be isolated, the splenocytes immortalized, and then screened for high affinity antibody binding. The immortalized cells, *e.g.* hybridomas, producing the desired antibodies may then be expanded. For further description, see Monoclonal Antibodies: A Laboratory Manual, Harlow and Lane eds., Cold Spring Harbor Laboratories, Cold Spring Harbor, New York, 1988. If desired, the mRNA encoding the heavy and light chains may be isolated and mutigenized by cloning in *E. coli*, and the heavy and light chains may be mixed to further enhance the affinity of the antibody. The antibodies may find use in diagnostic assays for detection of the presence of the PTC protein on the surface of cells or to inhibit the transduction of signal by the PTC protein ligand by competing for the binding site.

The mouse *patched* gene (SEQ ID NO:09) encodes a protein (SEQ ID NO:10) which has about 38% identical amino acids to fly PTC (SEQ ID NO:6) over about 1,200 amino acids. This amount of conservation is dispersed through much of the protein excepting the C-terminal region. The mouse protein also has a 50 amino acid insert relative to the fly protein. The human *patched* gene (SEQ ID NO:18) contains an open reading fram of about 1450 amino acids (SEQ ID NO:19) that is about 96% identical (98 % similar) to mouse *ptc* (SEQ ID NO:09). The human *patched* gene (SEQ ID NO:18), including coding and non-coding sequences, is about 89% identical to the mouse *patched* gene (SEQ ID NO:09).

The butterfly PTC homolog (SEQ ID NO:4) is 1,300 amino acids long and overall has a 50% amino acid identity (72% similarity) to fly PTC (SEQ ID NO:6). With the exception of a divergent C-terminus, this homology is evenly spread across the coding sequence. A 267bp exon from the beetle *patched* gene encodes an 89 amino acid protein fragment which was found to be 44% and 51% identical to the corresponding regions of fly and butterfly PTC respectively.

The mouse *ptc* message is about 8 kb long and the message is present in low levels as early as 7 dpc, the abundancy increasing by 11 and 15 dpc. Northern blot indicates a clear decrease in the amount of message at 17 dpc. In the adult, PTC

RNA is present in high amounts in the brain and lung, as well as in moderate amounts in the kidney and liver. Weak signals are detected in heart, spleen, skeletal muscle and testes.

In mouse embryos, *ptc* mRNA is present at 7 dpc, using *in situ* hybridization. *ptc* is present at high levels along the neural axis of 8.5 dpc embryos. By 11.5 dpc, *ptc* can be detected in developing lung buds and gut, consistent with its Northern profile. In addition, the gene is present at high levels in the ventricular zone of the central nervous system as well as in the zona limitans of the prosencephalon. *ptc* is also strongly transcribed in the perichondrium condensing cartilage of 11.5 and 13.5 dpc limb buds, as well as in the ventral portion of the somites, a region which is prospective sclerotome and eventually forms bone in the vertebral column. PTC is present in a wide range of tissues from endodermal, mesodermal, as well as ectodermal origin, evidencing the fundamental role in many aspects of embryonic development, including the condensation of cartilage, the patterning of limbs, the differentiation of lung tissue, and the generation of neurons.

The *patched* nucleic acid may be used for isolating the gene from various mammalian sources of interest, particularly primate, more particularly human, or from domestic animals, both pet and farm, *e.g.* lagomorpha, rodentiae, porcine, bovine, feline, canine, ovine, equine, etc. By using probes, particularly labeled probes of DNA sequences, of the *patched* gene, one may be able to isolate mRNA or genomic DNA, which may be then used for identifying mutations, particularly associated with genetic diseases, such as spina bifida, limb defects, lung defects, problems with tooth development, liver and kidney development, peripheral nervous system development, and other sites where a *patched* gene is involved in regulation. The subject probes can also be used for identifying the level of expression in cells associated with the testis to determine the relationship with the level of expression and sperm production.

The gene or fragments thereof may be used as probes for identifying the 5' non-coding region comprising the transcriptional initiation region, particularly the enhancer regulating the transcription of *patched*. By probing a genomic library, particularly with a probe comprising the 5' coding region, one can obtain fragments comprising the 5' non-coding region. If necessary, one may walk the fragment to

obtain further 5' sequence to ensure that one has at least a functional portion of the enhancer. It is found that the enhancer is proximal to the 5' coding region, a portion being in the transcribed sequence and downstream from the promoter sequences. The transcriptional initiation region may be used for many purposes, studying embryonic development, providing for regulated expression of *patched* protein or other protein of interest during embryonic development or thereafter, and in gene therapy.

The gene may also be used for gene therapy, by transfection of the normal gene into embryonic stem cells or into mature cells. A wide variety of viral vectors can be employed for transfection and stable integration of the gene into the genome of the cells. Alternatively, micro-injection may be employed, fusion, or the like for introduction of genes into a suitable host cell. *See*, for example, Dhawan *et al.*, Science 254, 1509-1512 (1991) and Smith *et al.*, Molecular and Cellular Biology (1990) 3268-3271.

By providing for the production of large amounts of PTC protein, one can use the protein for identifying ligands which bind to the PTC protein. Particularly, one may produce the protein in cells and employ the polysomes in columns for isolating ligands for the PTC protein. One may incorporate the PTC protein into liposomes by combining the protein with appropriate lipid surfactants, *e.g.* phospholipids, cholesterol, etc., and sonicate the mixture of the PTC protein and the surfactants in an aqueous medium. With one or more established ligands, *e.g.* *hedgehog*, one may use the PTC protein to screen for antagonists which inhibit the binding of the ligand. In this way, drugs may be identified which can prevent the transduction of signals by the PTC protein in normal or abnormal cells.

The PTC protein, particularly binding fragments thereof, the gene encoding the protein, or fragments thereof, particularly fragments of at least about 18 nucleotides, frequently of at least about 30 nucleotides and up to the entire gene, more particularly sequences associated with the hydrophilic loops, may be employed in a wide variety of assays. In these situations, the particular molecules will normally be joined to another molecule, serving as a label, where the label can directly or indirectly provide a detectable signal. Various labels include radioisotopes, fluorescers, chemiluminescers, enzymes, specific binding molecules,

particles, *e.g.* magnetic particles, and the like. Specific binding molecules include pairs, such as biotin and streptavidin, digoxin and antidigoxin etc. For the specific binding members, the complementary member would normally be labeled with a molecule which provides for detection, in accordance with known procedures. The assays may be used for detecting the presence of molecules which bind to the *patched* gene or PTC protein, in isolating molecules which bind to the *patched* gene, for measuring the amount of *patched*, either as the protein or the message, for identifying molecules which may serve as agonists or antagonists, or the like.

Various formats may be used in the assays. For example, mammalian or invertebrate cells may be designed where the cells respond when an agonist binds to PTC in the membrane of the cell. An expression cassette may be introduced into the cell, where the transcriptional initiation region of *patched* is joined to a marker gene, such as β-galactosidase, for which a substrate forming a blue dye is available. A 1.5kb fragment that responds to PTC signaling has been identified and shown to regulate expression of a heterologous gene during embryonic development. When an agonist binds to the PTC protein, the cell will turn blue. By employing a competition between an agonist and a compound of interest, absence of blue color formation will indicate the presence of an antagonist. These assays are well known in the literature. Instead of cells, one may use the protein in a membrane environment and determine binding affinities of compounds. The PTC may be bound to a surface and a labeled ligand for PTC employed. A number of labels have been indicated previously. The candidate compound is added with the labeled ligand in an appropriate buffered medium to the surface bound PTC. After an incubation to ensure that binding has occurred, the surface may be washed free of any non-specifically bound components of the assay medium, particularly any non-specifically bound labeled ligand, and any label bound to the surface determined. Where the label is an enzyme, substrate producing a detectable product may be used. The label may be detected and measured. By using standards, the binding affinity of the candidate compound may be determined.

The availability of the gene and the protein allows for investigation of the development of the fetus and the role *patched* and other molecules play in such development. By employing antisense sequences of the *patched* gene, where the

sequences may be introduced in cells in culture, or a vector providing for transcription of the antisense of the *patched* gene introduced into the cells, one can investigate the role the PTC protein plays in the cellular development. By providing for the PTC protein or fragment thereof in a soluble form which can compete with the normal cellular PTC protein for ligand, one can inhibit the binding of ligands to the cellular PTC protein to see the effect of variation in concentration of ligands for the PTC protein on the cellular development of the host. Antibodies against PTC can also be used to block function, since PTC is exposed on the cell surface.

The subject gene may also be used for preparing transgenic laboratory animals, which may serve to investigate embryonic development and the role the PTC protein plays in such development. By providing for variation in the expression of the PTC protein, employing different transcriptional initiation regions which may be constitutive or inducible, one can determine the developmental effect of the differences in PTC protein levels. Alternatively, one can use the DNA to knock out the PTC protein in embryonic stem cells, so as to produce hosts with only a single functional *patched* gene or where the host lacks a functional *patched* gene. By employing homologous recombination, one can introduce a *patched* gene, which is differentially regulated, for example, is expressed to the development of the fetus, but not in the adult. One may also provide for expression of the *patched* gene in cells or tissues where it is not normally expressed or at abnormal times of development. One may provide for mis-expression or failure of expression in certain tissue to mimic a human disease. Thus, mouse models of spina bifida or abnormal motor neuron differentiation in the developing spinal cord are made available. In addition, by providing expression of PTC protein in cells in which it is otherwise not normally produced, one can induce changes in cell behavior upon binding of ligand to the PTC protein.

Areas of investigation may include the development of cancer treatments. The *wingless* gene, whose transcription is regulated in flies by PTC, is closely related to a mammalian oncogene, *Wnt-1*, a key factor in many cases of mouse breast cancer. Other Wnt family members, which are secreted signaling proteins, are implicated in many aspects of development. In flies, the signaling factor *decapentaplegic*, a member of the TGF-beta family of signaling proteins, known to

affect growth and development in mammals, is also controlled by PTC. Since members of both the TGF-beta and Wnt families are expressed in mice in places close to overlapping with *patched*, the common regulation provides an opportunity in treating cancer. Also, for repair and regeneration, proliferation competent cells making PTC protein can find use to promote regeneration and healing for damaged tissue, which tissue may be regenerated by transfecting cells of damaged tissue with the *ptc* gene and its normal transcription initiation region or a modified transcription initiation region. For example, PTC may be useful to stimulate growth of new teeth by engineering cells of the gums or other tissues where PTC protein was during an earlier developmental stage or is expressed.

Since Northern blot analysis indicates that *ptc* is present at high levels in adult lung tissue, the regulation of *ptc* expression or binding to its natural ligand may serve to inhibit proliferation of cancerous lung cells. The availability of the gene encoding PTC and the expression of the gene allows for the development of agonists and antagonists. In addition, PTC is central to the ability of neurons to differentiate early in development. The availability of the gene allows for the introduction of PTC into host diseased tissue, stimulating the fetal program of division and/or differentiation. This could be done in conjunction with other genes which provide for the ligands which regulate PTC activity or by providing for agonists other than the natural ligand.

The availability of the coding region for various *ptc* genes from various species, allows for the isolation of the 5' non-coding region comprising the promoter and enhancer associated with the *ptc* genes, so as to provide transcriptional and post-transcriptional regulation of the *ptc* gene or other genes, which allow for regulation of genes in relation to the regulation of the *ptc* gene. Since the *ptc* gene is autoregulated, activation of the *ptc* gene will result in activation of transcription of a gene under the transcriptional control of the transcriptional initiation region of the *ptc* gene. The transcriptional initiation region may be obtained from any host species and introduced into a heterologous host species, where such initiation region is functional to the desired degree in the foreign host. For example, a fragment of from about 1.5 kb upstream from the initiation codon, up to about 10kb, preferably up to about 5 kb may be used to provide for transcriptional initiation regulated by

the PTC protein, particularly the *Drosophila* 5'-non-coding region (GenBank accession no. M28418).

The following examples are offered by illustration not by way of limitation.

EXPERIMENTAL

Methods and Materials

I. PCR on Mosquito (*Anopheles gambiae*) Genomic DNA:

PCR primers were based on amino acid stretches of fly PTC that were not likely to diverge over evolutionary time and were of low degeneracy. Two such primers (P2R1 (SEQ ID NO:14): GGACGAATTCAARGTNCAYCARYTNTGG, P4R1: (SEQ ID NO:15) GGACGAATTCCYTCCCARAARCANTC, (the underlined sequences are Eco RI linkers) amplified an appropriately sized band from mosquito genomic DNA using the PCR. The program conditions were as follows:

94 °C 4 min.; 72 °C Add Taq;

[49 °C 30 sec.; 72 °C 90 sec.; 94 °C 15 sec] 3 times

[94 °C 15 sec.; 50 °C 30 sec.; 72 °C 90 sec] 35 times

72 °C 10 min; 4 °C hold

This band was subcloned into the EcoRV site of pBluescript II and sequenced using the USB Sequence kit.

II. Screen of a Butterfly cDNA Library with Mosquito PCR Product

Using the mosquito PCR product (SEQ ID NO:7) as a probe, a 3 day embryonic *Precis coenia* λgt10 cDNA library (generously provided by Sean Carroll) was screened. Filters were hybridized at 65 °C overnight in a solution containing 5xSSC, 10% dextran sulfate, 5x Denhardt's, 200 μg/ml sonicated salmon sperm DNA, and 0.5% SDS. Filters were washed in 0.1X SSC, 0.1% SDS at room temperature several times to remove nonspecific hybridization. Of the 100,000 plaques initially screened, 2 overlapping clones, L1 and L2, were isolated, which corresponded to the N terminus of butterfly PTC. Using L2 as a probe, the library filters were rescreened and 3 additional clones (L5, L7, L8) were isolated which encompassed the remainder of the *ptc* coding sequence. The full length

sequence of butterfly *ptc* (SEQ ID NO:3) was determined by ABI automated sequencing.

III. Screen of a *Tribolium* (beetle) Genomic Library with Mosquito PCR Product and 900 bp Fragment from the Butterfly Clone

A λgem11 genomic library from *Tribolium casteneum* (gift of Rob Dennell) was probed with a mixture of the mosquito PCR (SEQ ID NO:7) product and BstXI/EcoRI fragment of L2. Filters were hybridized at 55 °C overnight and washed as above. Of the 75,000 plaques screened, 14 clones were identified and the SacI fragment of T8 (SEQ ID NO:1), which crosshybridized with the mosquito and butterfly probes, was subcloned into pBluescript.

IV. PCR on Mouse cDNA Using Degenerate Primers Derived from Regions Conserved in the Four Insect Homologues

Two degenerate PCR primers (P4REV: (SEQ ID NO:16) GGACGAATTCYTNGANTGYTTYTGGGA; P22: (SEQ ID NO:17) CATACCAGCCAAGCTTGTCIGGCCARTGCAT) were designed based on a comparison of PTC amino acid sequences from fly (*Drosophila melanogaster*) (SEQ ID NO:6), mosquito (*Anopheles gambiae*)(SEQ ID NO:8), butterfly (*Precis coenia*)(SEQ ID NO:4), and beetle (*Tribolium casteneum*)(SEQ ID NO:2). I represents inosine, which can form base pairs with all four nucleotides. P22 was used to reverse transcribe RNA from 12.5 dpc mouse limb bud (gift from David Kingsley) for 90 min at 37 °C. PCR using P4REV(SEQ ID NO:17) and P22(SEQ ID NO:18) was then performed on 1 μl of the resultant cDNA under the following conditions:

94 °C 4 min.; 72 °C Add Taq;
[94 °C 15 sec.; 50 °C 30 sec.; 72 °C 90 sec.] 35 times
72 °C 10 min.; 4 °C hold

PCR products of the expected size were subcloned into the TA vector (Invitrogen) and sequenced with the Sequenase Version 2.0 DNA Sequencing Kit (U.S.B.).

Using the cloned mouse PCR fragment as a probe, 300,000 plaques of a mouse 8.5 dpc λgt10 cDNA library (a gift from Brigid Hogan) were screened at

65 °C as above and washed in 2x SSC, 0.1% SDS at room temperature. 7 clones were isolated, and three (M2 M4, and M8) were subcloned into pBluescript II. 200,000 plaques of this library were rescreened using first, a 1.1 kb EcoRI fragment from M2 to identify 6 clones (M9-M16) and secondly a mixed probe containing the most N terminal (XhoI fragment from M2) and most C terminal sequences (BamHI/BglII fragment from M9) to isolate 5 clones (M17-M21). M9, M10, M14, and M17-21 were subcloned into the EcoRI site of pBluescript II (Strategene).

V. <u>RNA Blots and in situ Hybridizations in Whole and Sectioned Mouse Embryos</u>

Northerns:

A mouse embryonic Northern blot and an adult multiple tissue Northern blot (obtained from Clontech) were probed with a 900 bp EcoRI fragment from an N terminal coding region of mouse *ptc*. Hybridization was performed at 65 °C in 5x SSPE, 10x Denhardt's, 100 μg/ml sonicated salmon sperm DNA, and 2% SDS. After several short room temperature washes in 2x SSC, 0.05% SDS, the blots were washed at high stringency in 0.1X SSC, 0.1% SDS at 50C.

In situ hybridization of sections:

7.75, 8.5, 11.5, and 13.5 dpc mouse embryos were dissected in PBS and frozen in Tissue-Tek medium at -80 °C. 12-16 μm frozen sections were cut, collected onto VectaBond (Vector Laboratories) coated slides, and dried for 30-60 minutes at room temperature. After a 10 minute fixation in 4% paraformaldehyde in PBS, the slides were washed 3 times for 3 minutes in PBS, acetylated for 10 minutes in 0.25% acetic anhydride in triethanolamine, and washed three more times for 5 minutes in PBS. Prehybridization (50% formamide, 5X SSC, 250 μg/ml yeast tRNA, 500 μg/ml sonicated salmon sperm DNA, and 5x Denhardt's) was carried out for 6 hours at room temperature in 50% formamide/5x SSC humidified chambers. The probe, which consisted of 1 kb from the N-terminus of *ptc*, was added at a concentration of 200-1000 ng/ml into the same solution used for prehybridization, and then denatured for five minutes at 80 °C. Approximately 75 μl of probe were added to each slide and covered with Parafilm. The slides were incubated overnight at 65 °C in the same humidified chamber used previously. The following day, the probe was washed successively in 5X SSC (5 minutes, 65 °C),

0.2X SSC (1 hour, 65 °C), and 0.2X SSC (10 minutes, room temperature). After five minutes in buffer B1 (0.1M maleic acid, 0.15 M NaCl, pH 7.5), the slides were blocked for 1 hour at room temperature in 1% blocking reagent (Boerhinger-Mannheim) in buffer B1, and then incubated for 4 hours in buffer B1 containing the DIG-AP conjugated antibody (Boerhinger-Mannheim) at a 1:5000 dilution. Excess antibody was removed during two 15 minute washes in buffer B1, followed by five minutes in buffer B3 (100 mM Tris, 100mM NaCl, 5mM $MgCl_2$, pH 9.5). The antibody was detected by adding an alkaline phosphatase substrate (350 μl 75 mg/ml X-phosphate in DMF, 450 μl 50 mg/ml NBT in 70% DMF in 100 mls of buffer B3) and allowing the reaction to proceed over-night in the dark. After a brief rinse in 10 mM Tris, 1mM EDTA, pH 8.0, the slides were mounted with Aquamount (Lerner Laboratories).

VI. <u>*Drosophila* 5-transcriptional initiation region β-gal constructs</u>.

A series of constructs were designed that link different regions of the *ptc* promoter from *Drosophila* to a *LacZ* reporter gene in order to study the cis regulation of the *ptc* expression pattern. See Fig. 1. A 10.8kb BamHI/BspM1 fragment comprising the 5'-non-coding region of the mRNA at its 3'-terminus was obtained and truncated by restriction enzyme digestion as shown in Fig. 1. These expression cassettes were introduced into *Drosophila* lines using a P-element vector (Thummel et al., Gene 74, 445-456 (1988), which were injected into embryos, providing flies which could be grown to produce embryos. (*See* Spradling and Rubin, Science (1982) 218, 341-347 for a description of the procedure.) The vector used a pUC8 background into which was introduced the white gene to provide for yellow eyes, portions of the P-element for integrtion, and the constructs were inserted into a polylinker upstream from the *LacZ* gene. The resulting embryos were stained using antibodies to LacZ protein conjugated to HRP and the embryos developed with OPD dye to identify the expression of the *LacZ* gene. The staining pattern is described in Fig. 1, indicating whether there was staining during the early and late development of the embryo.

VII. <u>Isolation of a Mouse *ptc* Gene</u>

Homologues of fly PTC (SEQ ID NO:6) were isolated from three insects: mosquito, butterfly and beetle, using either PCR or low stringency library screens. PCR primers to six amino acid stretches of PTC of low mutatability and degeneracy were designed. One primer pair, P2 and P4, amplified an homologous fragment of *ptc* from mosquito genomic DNA that corresponded to the first hydrophilic loop of the protein. The 345bp PCR product (SEQ ID NO:7) was subcloned and sequenced and when aligned to fly PTC, showed 67% amino acid identity.

The cloned mosquito fragment was used to screen a butterfly λGT 10 cDNA library. Of 100,000 plaques screened, five overlapping clones were isolated and used to obtain the full length coding sequence. The butterfly PTC homologue (SEQ ID NO:4) is 1,311 amino acids long and overall has 50% amino acid identity (72% similarity) to fly PTC. With the exception of a divergent C-terminus, this homology is evenly spread across the coding sequence. The mosquito PCR clone (SEQ ID NO:7) and a corresponding fragment of butterfly cDNA were used to screen a beetle λgem11 genomic library. Of the plaques screened, 14 clones were identified. A fragment of one clone (T8), which hybridized with the original probes, was subcloned and sequenced. This 3kb piece contains an 89 amino acid exon (SEQ ID NO:2) which is 44% and 51% identical to the corresponding regions of fly and butterfly PTC respectively.

Using an alignment of the four insect homologues in the first hydrophilic loop of the PTC, two PCR primers were designed to a five and six amino acid stretch which were identical and of low degeneracy. These primers were used to isolate the mouse homologue using RT-PCR on embryonic limb bud RNA. An appropriately sized band was amplified and upon cloning and sequencing, it was found to encode a protein 65% identical to fly PTC. Using the cloned PCR product and subsequently, fragments of mouse *ptc* cDNA, a mouse embryonic λcDNA library was screened. From about 300,000 plaques, 17 clones were identified and of these, 7 form overlapping cDNA's which comprise most of the protein-coding sequence (SEQ ID NO:9).

VIIa. Developmental and Tissue Distribution of Mouse PTC RNA

In both the embryonic and adult Northern blots, the *ptc* probe detects a single 8kb message. Further exposure does not reveal any additional minor bands. Developmentally, *ptc* mRNA is present in low levels as early as 7 dpc and becomes quite abundant by 11 and 15 dpc. While the gene is still present at 17 dpc, the Northern blot indicates a clear decrease in the amount of message at this stage. In the adult, *ptc* RNA is present in high amounts in the brain and lung, as well as in moderate amounts in the kidney and liver. Weak signals are detected in heart, spleen, skeletal muscle, and testes.

VIIb. *In situ* Hybridization of Mouse PTC in Whole and Section Embryos

Northern analysis indicates that *ptc* mRNA is present at 7 dpc, while there is no detectable signal in sections from 7.75 dpc embryos. This discrepancy is explained by the low level of transcription. In contrast, *ptc* is present at high levels along the neural axis of 8.5 dpc embryos. By 11.5 dpc, *ptc* can be detected in the developing lung buds and gut, consistent with its adult Northern profile. In addition, the gene is present at high levels in the ventricular zone of the central nervous system, as well as in the zona limitans of the prosencephalon. *ptc* is also strongly transcribed in the condensing cartilage of 11.5 and 13.5 dpc limb buds, as well as in the ventral portion of the somites, a region which is prospective sclerotome and eventually forms bone in the vertebral column. *ptc* is present in a wide range of tissues from endodermal, mesodermal and ectodermal origin supporting its fundamental role in embryonic development.

VIII. Isolation of the Human *ptc* Gene

To isolate human *ptc* (hptc), 2 x 10^5 plaques from a human lung cDNA library (HL3022a, Clonetech) were screened with a 1kbp mouse *ptc* fragment, M2-2. Filters were hybridized overnight at reduced stringency (60 °C in 5X SSC, 10% dextran sulfate, 5X Denhardt's, 0.2 mg/ml sonicated salmon sperm DNA, and 0.5% SDS). Two positive plaques (H1 and H2) were isolated, the inserts cloned into pBluescript, and upon sequencing, both contained sequence highly similar to the mouse ptc homolog. To isolate the 5' end, an additional 6 x 10^5 plaques were screened in duplicate with M2-3 EcoR I and M2-3 Xho I (containing 5' untranslated

sequence of mouse *ptc*) probes. Ten plaques were purified and of these, 6 inserts were subloned into pBluescript. To obtain the full coding sequence, H2 was fully and H14, H20, and H21 were partially sequenced. The 5.1kbp of human *ptc* sequence (SEQ ID NO:18) contains an open reading frame of 1447 amino acids (SEQ ID NO:19) that is 96% identical and 98% similar to mouse *ptc*. The 5' and 3' untranslated sequences of human *ptc* (SEQ ID NO:18) are also highly similar to mouse *ptc* (SEQ ID NO:09) suggesting conserved regulatory sequence.

IX. Comparison of Mouse, Human, Fly and Butterfly Sequences

The deduced mouse PTC protein sequence (SEQ ID NO:10) has about 38% identical amino acids to fly PTC over about 1,200 amino acids. This amount of conservation is dispersed through much of the protein excepting the C-terminal region. The mouse protein also has a 50 amino acid insert relative to the fly protein. Based on the sequence conservation of PTC and the functional conservation of *hedgehog* between fly and mouse, one concludes that *ptc* functions similarly in the two organisms. A comparison of the amino acid sequences of mouse (mptc) (SEQ ID NO:10), human (hptc) (SEQ ID NO:19), butterfly (bptc)(SEQ ID NO:4) and drosophila (ptc) (SEQ ID NO:6) is shown in Table 1.

TABLE 1

alignment of human, mouse, fly, and butterfly PTC homologs

```
                    alignment of human, mouse, fly, and butterfly ptc homologs

HPTC       MASAGNAAEPQDR--GGGGSGCIGAPGRPAGGGRRRRTGGLRRAAAPDRDYLHRPSYCDA
MPTC       MASAGNAA---------------GALGRQAGGGRRRRTGGPHRA-APDRDYLHRPSYCDA
PTC        M-----DRDSLPRVPDTHGD--VVDE---------KLFSDL---------YI-RTSWVDA
BPTC       MVAPDSEAPSNPRITAAHESPCATEA---------RHSADL---------YI-RTSWVDA
           *
                                              .   ..          *. * *  **

HPTC       AFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGAFAVGLKA
MPTC       AFALEQISKGKATGRKAPLWLRAKFQRLLFKLGCYIQKNCGKFLVVGLLIFGAFAVGLKA
PTC        QVALDQIDKGKARGSRTAIYLRSVFQSHLETLGSSVQKHAGKVLFVAILVLSTFCVGLKS
BPTC       ALALSELEKGNIEGGRTSLWIRAWLQEQLFILGCFLQGDAGKVLFVAILVLSTFCVGLKS
             **  ..  **.   *  .... .*. .*  *  **   .*  . ** * *..*....* ****.

HPTC       ANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLTTEALLQH
MPTC       ANLETNVEELWVEVGGRVSRELNYTRQKIGEEAMFNPQLMIQTPKEEGANVLTTEALLQH
PTC        AQIHSKVHQLWIQEGGRLEAELAYTQKTIGEDESATHQLLIQTTHDPNASVLHPQALLAH
BPTC       AQIHTRVDQLWVQEGGRLEAELKYTAQALGEADSSTHQLVIQTAKDPDVSLLHPGALLEH
           *.... *..**.. ***.  ** **  . .**        **.***   .    ..*   *** *

HPTC       LDSALQASRVHVYMYNRQWKLEHLCYKSGELITET-GYMDQIIEYLYPCLIITPLDCFWE
```

```
MPTC   LDSALQASRVHVYMYNRQWKLEHLCYKSGELITET-GYMDQIIEYLYPCLIITPLDCFWE
PTC    LEVLVKATAVKVHLYDTEWGLRDMCNMPSTPSFEGIYYIEQILRHLIPCSIITPLDCFWE
BPTC   LKVVHAATRVTVHMYDIEWRLKDLCYSPSIPDFEGYHHIESIIDNVIPCAIITPLDCFWE
       *     *. * * .*. .* * ..*  ..     *       .. *.  . ** **********

HPTC   GAKLQSGTAYLLGKPPLR----WTNFDPLEFLEELK------KINYQVDSWEEMLNKAEV
MPTC   GAKLQSGTAYLLGKPPLR----WTNFDPLEFLEELK------KINYQVDSWEEMLNKAEV
PTC    GSQLL-GPESAVVIPGLNQRLLWTTLNPASVMQYMKQKMSEEKISFDFETVEQYMKRAAI
BPTC   GSKLL-GPDYPIYVPHLKHKLQWTHLNPLEVVEEVK-KL---KFQFPLSTIEAYMKRAGI
        *..*  *    .  * *     ** ..*    .. .*      *. .    .  *   ...* .

HPTC   GHGYMDRPCLNPADPDCPATAPNKNSTKPLDMALVLNGGCHGLSRKYMHWQEELIVGGTV
MPTC   GHGYMDRPCLNPADPDCPATAPNKNSTKPLDVALVLNGGCQGLSRKYMHWQEELIVGGTV
PTC    GSGYMEKPCLNPLNPNCPDTAPNKNSTQPPDVGAILSGGCYGYAAKHMHWPEELIVGGRK
BPTC   TSAYMKKPCLDPTDPHCPATAPNKKSGHIPDVAAELSHGCYGFAAAYMHWPEQLIVGGAT
        .** .***.* .*.** *****.*     *..   *. ** *  .     *** *.*****

HPTC   KNSTGKLVSAHALQTMFQLMTPKQMYEHFKGYEYVSHINWNEDKAAAILEAWQRTYVEVV
MPTC   KNATGKLVSAHALQTMFQLMTPKQMYEHFRGYDYVSHINWNEDRAAAILEAWQRTYVEVV
PTC    RNRSGHLRKAQALQSVVQLMTEKEMYDQWQDNYKVHHLGWTQEKAAEVLNAWQRNFSREV
BPTC   RNSTSALRSARALQTVVQLMGEREMYEYWADHYKVHQIGWNQEKAAAVLDAWQRKFAAEV
       .* .. *  *.***.. ***  ..**.     .    * .. * ...** .*.****  .   *

HPTC   HQSVAQNSTQK----VLSFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRW-DC
MPTC   HQSVAPNSTQK----VLPFTTTTLDDILKSFSDVSVIRVASGYLLMLAYACLTMLRW-DC
PTC    EQLLRKQSRIATNYDIYVFSSAALDDILAKFSHPSALSIVIGVAVTVLYAFCTLLRWRDP
BPTC   RKI-TTSGSVSSAYSFYPFSTSTLNDILGKFSEVSLKNIILGYMFMLIYVAVTLIQWRDP
                          *....*.***  **. *    .   *     . *    *...* *
        .      .

HPTC   SKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAF
MPTC   SKSQGAVGLAGVLLVALSVAAGLGLCSLIGISFNAATTQVLPFLALGVGVDDVFLLAHAF
PTC    VRGQSSVGVAGVLLMCFSTAAGLGLSALLGIVFNAASTQVVPFLALGLGVDHIFMLTAAY
BPTC   IRSQAGVGIAGVLLLSITVAAGLGFCALLGIPFNASSTQIVPFLALGLGVQDMFLLTHTY
        ..*..**.*****.  ..  *****.  .*.** ***..**..******.**...*.*.  ..

HPTC   SETGQNKRIPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVV
MPTC   SETGQNKRIPFEDRTGECLKRTGASVALTSISNVTAFFMAALIPIPALRAFSLQAAVVVV
PTC    AESN------RREQTKLILKKVGPSILFSACSTAGSFFAAAFIPVPALKVFCLQAAIVMC
BPTC   VEQAGD--VPREERTGLVLKKSGLSVLLASLCNVMAFLAAALLPIPAFRVFCLQAAILLL
        *            ..*    **. * *. ...       .*. **..*.**.. * ****...

HPTC   FNFAMVLLIFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTDTHDNTRYSPP
MPTC   FNFAMVLLIFPAILSMDLYRREDRRLDIFCCFTSPCVSRVIQVEPQAYTEPHSNTRYSPP
PTC    SNLAAALLVFPAMISLDLRRRTAGRADIFCCCF-PVWKEQPKVAPPVLPLNNNNGR----
BPTC   FNLGSILLVFPAMISLDLRRRSAARADLLCCLM-P---ESP------LPKKKIPER----
        *..  **.***..*.** **   * *..**    *                        *

HPTC   PPYSSHSFAHETQITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDT LSCQSP
MPTC   PPYTSHSFAHETHITMQSTVQLRTEYDPHTHVYYTTAEPRSEISVQPVTVTQDNLSCQSP
PTC    ----------------------------------GARHPKSCNNNRVPLPAQNPLLEQRA
BPTC   ----------------------------------AKTRKNDKTHRID-TTRQPLDPDVS
                                          .   ..    .     ... *  . .

HPTC   ESTSSTRDLLSQFSDSSLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVIFLFLGLLG
MPTC   ESTSSTRDLLSQFSDSSLHCLEPPCTKWTLSSFAEKHYAPFLLKPKAKVVVILLFLGLLG
PTC    DIPGSS------------HSLASF----SLATFAFQHYTPFLMRSWVKFLTVMGFLAALI
BPTC   ENVTKT------------CCL-SV----SLTKWAKNQYAPFIMRPAVKVTSMLALIAVIL
                          * .     .*.  *  ..*.**....   *    .   ... .
        .     .

HPTC   VSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYD
MPTC   VSLYGTTRVRDGLDLTDIVPRETREYDFIAAQFKYFSFYNMYIVTQKA-DYPNIQHLLYD
PTC    SSLYASTRLQDGLDIIDLVPKDSNEHKFLDAQTRLFGFYSMYAVTQGNFEYPTQQQLLRD
BPTC   TSVWGATKVKDGLDLTDIVPENTDEHEFLSRQEKYFGFYNMYAVTQGNFEYPTNQKLLYE
        *. ..*...****. *.** .. *  *.  *  . *.**.** ***    .**  * ** .
```

```
HPTC   LHRSFSNVKYVMLEENKQLPKMWLHYFRDWLQGLQDAFDSDWETGKIMPNN-YKNGSDDG
MPTC   LHKSFSNVKYVMLEENKQLPQMWLHYFRDWLQGLQDAFDSDWETGRIMPNN-YKNGSDDG
PTC    YHDSFVRVPHVIKNDNGGLPDFWLLLFSEWLGNLQKIFDEEYRDGRLTKECWFPNASSDA
BPTC   YHDQFVRIPNIIKNDNGGLTKFWLSLFRDWLLDLQVAFDKEVASGCITQEYWCKNASDEG
        *  *   .  .. ..*  *   **  * .**  **  **  .   *  .  .   *.* ..

HPTC   VLAYKLLVQTGSRDKPIDISQLTK-QRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQA
MPTC   VLAYKLLVQTGSRDKPIDISQLTK-QRLVDADGIINPSAFYIYLTAWVSNDPVAYAASQA
PTC    ILAYKLIVQTGHVDNPVDKELVLT-NRLVNSDGIINQRAFYNYLSAWATNDVFAYGASQG
BPTC   ILAYKLMVQTGHVDNPIDKSLITAGHRLVDKDGIINPKAFYNYLSAWATNDALAYGASQG
       .*****.****  *.*.*   .   .***. *****  *** **.** .**  **.***.

HPTC   NIRPHRPEWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRTICS
MPTC   NIRPHRPEWVHDKADYMPETRLRIPAAEPIEYAQFPFYLNGLRDTSDFVEAIEKVRVICN
PTC    KLYPEPRQYFHQPNEY----DLKIPKSLPLVYAQMPFYLHGLTDTSQIKTLIGHIRDLSV
BPTC   NLKPQPQRWIHSPEDV----HLEIKKSSPLIYTQLPFYLSGLSDTDSIKTLIRSVRDLCL
       .. *.    *    .      * *  . *. *.* **** ** **    .    *  .* .

HPTC   NYTSLGLSSYPNGYPFLFWEQYIGLRHWLLLFISVVLACTFLVCAVFLLNPWTAGIIVMV
MPTC   NYTSLGLSSYPNGYPFLFWEQYISLRHWLLLSISVVLACTFLVCAVFLLNPWTAGIIVMV
PTC    KYEGFGLPNYPSGIPFIFWEQYMTLRSSLAMILACVLLAALVLVSLLLLSVWAAVLVILS
BPTC   KYEAKGLPNFPSGIPFLFWEQYLYLRTSLLLALACALGAVFIAVMVLLLNAWAAVLVTLA
       .*  . **...*.* **.*****. **  *  . ..  *   ..   ..**. *.* .. .

HPTC   LALMTVELFGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNRRAVLAL
MPTC   LALMTVELFGMMGLIGIKLSAVPVVILIASVGIGVEFTVHVALAFLTAIGDKNHRAMLAL
PTC    VLASLAQIFGAMTLLGIKLSAIPAVILILSVGMMLCFNVLISLGFMTSVGNRQRRVQLSM
BPTC   LATLVLQLLGVMALLGVKLSAMPPVLLVLAIGRGVHFTVHLCLGFVTSIGCKRRRASLAL
       .    ...* * *.*.****.* ***. ..*  . * * . *.*.*..* . .*  *..

HPTC   EHMFAPVLDGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTILGVLNGLVLLPVLLSFFG
MPTC   EHMFAPVLDGAVSTLLGVLMLAGSEFDFIVRYFFAVLAILTVLGVLNGLVLLPVLLSFFG
PTC    QMSLGPLVHGMLTSGVAVFMLSTSPFEFVIRHFCWLLLVVLCVGACNSLLVFPILLSMVG
BPTC   ESVLAPVVHGALAAAALAASMLAASEFGFVARLFLRLLLALVFLGLIDGLLFFPIVLSILG
       .  ..*...*  ... ..  **. * * *. * *  .*  .  .*  ..*. .*..** *

HPTC   PYPEVSPANGLNRLPTPSPEPPPSVVRFAMPPGHTHSGSDSSDSEYSSQTTVSGLSE-EL
MPTC   PCPEVSPANGLNRLPTPSPEPPPSVVRFAVPPGHTNNGSDSSDSEYSSQTTVSGISE-EL
PTC    PEAELVPLEHPDRISTPSPLPVRSSKRSGKSYVVQGSRSSRGSCQKSHHHHHKDLNDPSL
BPTC   PAAEVRPIEHPERLSTPSPKCSPIHPRKSSSSSGGGDKSSRTS--KSAPRPC----APSL
       * .*. *  .  .*..****              * . .       *       *    *

HPTC   RHYEAQQGAGGPAHQVIVEATENPVFAHSTVVHPESRHHPPSNPRQQPHLDSGSLPPGRQ
MPTC   RQYEAQQGAGGPAHQVIVEATENPVFARSTVVHPDSRHQPPLTPRQQPHLDSGSLSPGRQ
PTC    TTITEEPQSWKSSNSSIQMPNDWTYQPREQ--RPASYAAPPPAYHKAAAQQHHQHQGPPT
BPTC   TTITEEPSSWHSSAHSVQSSMQSIVVQPEVVVETTTYNGSDSASGRSTPTKSSHGGAITT
          .   .   ..   .   .  .                     .     .     .

HPTC   GQQPRRDPPREGLWPPLYRPRRDAFEISTEGHSGPSNRARWGPRGARSHNPRNPASTAMG
MPTC   GQQPRRDPPREGLRPPPYRPRRDAFEISTEGHSGPSNRDRSGPRGARSHNPRNPTSTAMG
PTC    TPPPPFPTA-----------------YPPELQSIVVQPEVTVETTHS-----------DS
BPTC   TKVTATANIKVEVVTPSDRKSRRSYHYYDRRRDRDEDRDRDRERDRDRDRDRDRDRDRDR
                                                      .    .

HPTC   SSVPGYCQPITTVTASASVTVAVHPPPVPGPGRNPRGGLCPGY---PETDHGLFEDPHVP
MPTC   SSVPSYCQPITTVTASASVTVAVHPP--PGPGRNPRGGPCPGYESYPETDHGVFEDPHVP
PTC    NT--------TKVTATANIKVELAMP-----GRAVRS---YNFTS---------------
BPTC   DR--------DRERSRERDRRDRYRD-----ERDHRA---SPRENGRDSGHE--------
                        .                    *  *.

HPTC   FHVRCERRDSKVEVIELQDVECEERPRGSSSN
MPTC   FHVRCERRDSKVEVIELQDVECEERPWGSSSN
PTC    --------------------------------
BPTC   --------------------------SDSSRH
```

The identity of ten other clones recovered from the mouse library is not determined. These cDNAs cross-hybridize with mouse *ptc* sequence, while differing as to their restriction maps. These genes encode a family of proteins related to the *patched* protein. Alignment of the human and mouse nucleotide sequences, which includes coding and noncoding sequence, reveals 89% identity.

In accordance with the subject invention, mammalian *patched* genes, including the mouse and human genes, are provided which allow for high level production of the *patched* protein, which can serve many purposes. The *patched* protein may be used in a screening for agonists and antagonists, for isolation of its ligand, particularly *hedgehog*, more particularly *Sonic hedgehog*, and for assaying for the transcription of the mRNA *ptc*. The protein or fragments thereof may be used to produce antibodies specific for the protein or specific epitopes of the protein. In addition, the gene may be employed for investigating embryonic development, by screening fetal tissue, preparing transgenic animals to serve as models, and the like.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it will be readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE BOARD OF TRUSTEES OF THE LELAND STANFORD JUNIOR UNIVERSITY

(ii) TITLE OF INVENTION: Patched Genes and their Use

(iii) NUMBER OF SEQUENCES: 19

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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US95/
(B) FILING DATE: 06-OCT-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Rowland, Bertram I
(B) REGISTRATION NUMBER: 20015
(C) REFERENCE/DOCKET NUMBER: a60190-1

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 415-781-1989
(B) TELEFAX: 415-398-3249

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 736 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AACNNCNNTN NATGGCACCC CCNCCCAACC TTTNNNCCNN NTAANCAAAA NNCCCCNTTT 60

NATACCCCCT NTAANANTTT TCCACCNNNC NNAAANNCCN CTGNANACNA NGNAAANCCN 120

TTTTTNAACC CCCCCCACCC GGAATTCCNA NTNNCCNCCC CCAAATTACA ACTCCAGNCC 180

AAAATTNANA NAATTGGTCC TAACCTAACC NATNGTTGTT ACGGTTTCCC CCCCCAAATA 240

CATGCACTGG CCCGAACACT TGATCGTTGC CGTTCCAATA AGAATAAATC TGGTCATATT 300

AAACAAGCCN AAAGCTTTAC AAACTGTTGT ACAATTAATG GGCGAACACG AACTGTTCGA 360

ATTCTGGTCT GGACATTACA AAGTGCACCA CATCGGATGG AACCAGGAGA AGGCCACAAC 420

CGTACTGAAC GCCTGGCAGA AGAAGTTCGC ACAGGTTGGT GGTTGGCGCA AGGAGTAGAG 480

TGAATGGTGG TAATTTTTGG TTGTTCCAGG AGGTGGATCG TCTGACGAAG AGCAAGAAGT 540

CGTCGAATTA CATCTTCGTG ACGTTCTCCA CCGCCAATTT GAACAAGATG TTGAAGGAGG 600

CGTCGAANAC GGACGTGGTG AAGCTGGGGG TGGTGCTGGG GGTGGCGGCG GTGTACGGGT 660

GGGTGGCCCA GTCGGGGCTG GCTGCCTTGG GAGTGCTGGT CTTNGCGNGC TNCNATTCGC 720

CCTATAGTNA GNCGTA 736

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 107 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Xaa Pro Pro Pro Asn Tyr Asn Ser Xaa Pro Lys Xaa Xaa Xaa Leu Val
1 5 10 15

Leu Thr Pro Xaa Val Val Thr Val Ser Pro Pro Lys Tyr Met His Trp
20 25 30

Pro Glu His Leu Ile Val Ala Val Pro Ile Arg Ile Asn Leu Val Ile
35 40 45

Leu Asn Lys Pro Lys Ala Leu Gln Thr Val Val Gln Leu Met Gly Glu
50 55 60

His Glu Leu Phe Glu Phe Trp Ser Gly His Tyr Lys Val His His Ile
65 70 75 80

Gly Trp Asn Gln Glu Lys Ala Thr Thr Val Leu Asn Ala Trp Gln Lys
85 90 95

Lys Phe Ala Gln Val Gly Gly Trp Arg Lys Glu

100 105

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGTCTGTCA CCCGGAGCCG GAGTCCCCGG CGGCCAGCAG CGTCCTCGCG AGCCGAGCGC 60

CCAGGCGCGC CCGGAGCCCG CGGCGGCGGC GGCAACATGG CCTCGGCTGG TAACGCCGCC 120

GGGGCCCTGG GCAGGCAGGC CGGCGGCGGG AGGCGCAGAC GGACCGGGGG ACCGCACCGC 180

GCCGCGCCGG ACCGGGACTA TCTGCACCGG CCCAGCTACT GCGACGCCGC CTTCGCTCTG 240

GAGCAGATTT CCAAGGGGAA GGCTACTGGC CGGAAAGCGC CGCTGTGGCT GAGAGCGAAG 300

TTTCAGAGAC TCTTATTTAA ACTGGGTTGT TACATTCAAA AGAACTGCGG CAAGTTTTTG 360

GTTGTGGGTC TCCTCATATT TGGGGCCTTC GCTGTGGGAT TAAAGGCAGC TAATCTCGAG 420

ACCAACGTGG AGGAGCTGTG GGTGGAAGTT GGTGGACGAG TGAGTCGAGA ATTAAATTAT 480

ACCCGTCAGA AGATAGGAGA AGAGGCTATG TTTAATCCTC AACTCATGAT ACAGACTCCA 540

AAAGAAGAAG GCGCTAATGT TCTGACCACA GAGGCTCTCC TGCAACACCT GGACTCAGCA 600

CTCCAGGCCA GTCGTGTGCA CGTCTACATG TATAACAGGC AATGGAAGTT GGAACATTTG 660

TGCTACAAAT CAGGGGAACT TATCACGGAG ACAGGTTACA TGGATCAGAT AATAGAATAC 720

CTTTACCCTT GCTTAATCAT TACACCTTTG GACTGCTTCT GGGAAGGGGC AAAGCTACAG 780

TCCGGGACAG CATACCTCCT AGGTAAGCCT CCTTTACGGT GGACAAACTT TGACCCCTTG 840

GAATTCCTAG AAGAGTTAAA GAAAATAAAC TACCAAGTGG ACAGCTGGGA GGAAATGCTG 900

AATAAAGCCG AAGTTGGCCA TGGGTACATG GACCGGCCTT GCCTCAACCC AGCCGACCCA 960

GATTGCCCTG CCACAGCCCC TAACAAAAAT TCAACCAAAC CTCTTGATGT GGCCCTTGTT 1020

TTGAATGGTG GATGTCAAGG TTTATCCAGG AAGTATATGC ATTGGCAGGA GGAGTTGATT 1080

GTGGGTGGTA CCGTCAAGAA TGCCACTGGA AAACTTGTCA GCGCTCACGC CCTGCAAACC 1140

ATGTTCCAGT TAATGACTCC CAAGCAAATG TATGAACACT TCAGGGGCTA CGACTATGTC 1200

TCTCACATCA ACTGGAATGA AGACAGGGCA GCCGCCATCC TGGAGGCCTG GCAGAGGACT 1260

TACGTGGAGG TGGTTCATCA AAGTGTCGCC CCAAACTCCA CTCAAAAGGT GCTTCCCTTC 1320

ACAACCACGA CCCTGGACGA CATCCTAAAA TCCTTCTCTG ATGTCAGTGT CATCCGAGTG 1380

GCCAGCGGCT ACCTACTGAT GCTTGCCTAT GCCTGTTTAA CCATGCTGCG CTGGGACTGC 1440

TCCAAGTCCC AGGGTGCCGT GGGGCTGGCT GGCGTCCTGT TGGTTGCGCT GTCAGTGGCT 1500

GCAGGATTGG GCCTCTGCTC CTTGATTGGC ATTTCTTTTA ATGCTGCGAC AACTCAGGTT 1560

TTGCCGTTTC TTGCTCTTGG TGTTGGTGTG GATGATGTCT TCCTCCTGGC CCATGCATTC 1620

AGTGAAACAG GACAGAATAA GAGGATTCCA TTTGAGGACA GGACTGGGGA GTGCCTCAAG 1680

CGCACCGGAG CCAGCGTGGC CCTCACCTCC ATCAGCAATG TCACCGCCTT CTTCATGGCC 1740

GCATTGATCC CTATCCCTGC CCTGCGAGCG TTCTCCCTCC AGGCTGCTGT GGTGGTGGTA 1800

TTCAATTTTG CTATGGTTCT GCTCATTTTT CCTGCAATTC TCAGCATGGA TTTATACAGA 1860

CGTGAGGACA GAAGATTGGA TATTTTCTGC TGTTTCACAA GCCCCTGTGT CAGCAGGGTG 1920

ATTCAAGTTG AGCCACAGGC CTACACAGAG CCTCACAGTA ACACCCGGTA CAGCCCCCCA 1980

CCCCCATACA CCAGCCACAG CTTCGCCCAC GAAACCCATA TCACTATGCA GTCCACCGTT 2040

CAGCTCCGCA CAGAGTATGA CCCTCACACG CACGTGTACT ACACCACCGC CGAGCCACGC 2100

TCTGAGATCT CTGTACAGCC TGTTACCGTC ACCCAGGACA ACCTCAGCTG TCAGAGTCCC 2160

GAGAGCACCA GCTCTACCAG GGACCTGCTC TCCCAGTTCT CAGACTCCAG CCTCCACTGC 2220

CTCGAGCCCC CCTGCACCAA GTGGACACTC TCTTCGTTTG CAGAGAAGCA CTATGCTCCT 2280

TTCCTCCTGA AACCCAAAGC CAAGGTTGTG GTAATCCTTC TTTTCCTGGG CTTGCTGGGG 2340

GTCAGCCTTT ATGGGACCAC CCGAGTGAGA GACGGGCTGG ACCTCACGGA CATTGTTCCC 2400

CGGGAAACCA GAGAATATGA CTTCATAGCT GCCCAGTTCA AGTACTTCTC TTTCTACAAC 2460

ATGTATATAG TCACCCAGAA AGCAGACTAC CCGAATATCC AGCACCTACT TTACGACCTT 2520

CATAAGAGTT TCAGCAATGT GAAGTATGTC ATGCTGGAGG AGAACAAGCA ACTTCCCCAA 2580

ATGTGGCTGC ACTACTTTAG AGACTGGCTT CAAGGACTTC AGGATGCATT TGACAGTGAC 2640

TGGGAAACTG GGAGGATCAT GCCAAACAAT TATAAAAATG GATCAGATGA CGGGGTCCTC 2700

GCTTACAAAC TCCTGGTGCA GACTGGCAGC CGAGACAAGC CCATCGACAT TAGTCAGTTG 2760

ACTAAACAGC GTCTGGTAGA CGCAGATGGC ATCATTAATC CGAGCGCTTT CTACATCTAC 2820

CTGACCGCTT GGGTCAGCAA CGACCCTGTA GCTTACGCTG CCTCCCAGGC CAACATCCGG 2880

CCTCACCGGC CGGAGTGGGT CCATGACAAA GCCGACTACA TGCCAGAGAC CAGGCTGAGA 2940

ATCCCAGCAG CAGAGCCCAT CGAGTACGCT CAGTTCCCTT TCTACCTCAA CGGCCTACGA 3000

GACACCTCAG ACTTTGTGGA AGCCATAGAA AAAGTGAGAG TCATCTGTAA CAACTATACG 3060
AGCCTGGGAC TGTCCAGCTA CCCCAATGGC TACCCCTTCC TGTTCTGGGA GCAATACATC 3120
AGCCTGCGCC ACTGGCTGCT GCTATCCATC AGCGTGGTGC TGGCCTGCAC GTTTCTAGTG 3180
TGCGCAGTCT TCCTCCTGAA CCCCTGGACG GCCGGGATCA TTGTCATGGT CCTGGCTCTG 3240
ATGACCGTTG AGCTCTTTGG CATGATGGGC CTCATTGGGA TCAAGCTGAG TGCTGTGCCT 3300
GTGGTCATCC TGATTGCATC TGTTGGCATC GGAGTGGAGT TCACCGTCCA CGTGGCTTTG 3360
GCCTTTCTGA CAGCCATTGG GGACAAGAAC CACAGGGCTA TGCTCGCTCT GGAACACATG 3420
TTTGCTCCCG TTCTGGACGG TGCTGTGTCC ACTCTGCTGG GTGTACTGAT GCTTGCAGGG 3480
TCCGAATTTG ATTTCATTGT CAGATACTTC TTTGCCGTCC TGGCCATTCT CACCGTCTTG 3540
GGGGTTCTCA ATGGACTGGT TCTGCTGCCT GTCCTCTTAT CCTTCTTTGG ACCGTGTCCT 3600
GAGGTGTCTC CAGCCAATGG CCTAAACCGA CTGCCCACTC CTTCGCCTGA GCCGCCTCCA 3660
AGTGTCGTCC GGTTTGCCGT GCCTCCTGGT CACACGAACA ATGGGTCTGA TTCCTCCGAC 3720
TCGGAGTACA GCTCTCAGAC CACGGTGTCT GGCATCAGTG AGGAGCTCAG GCAATACGAA 3780
GCACAGCAGG GTGCCGGAGG CCCTGCCCAC CAAGTGATTG TGGAAGCCAC AGAAAACCCT 3840
GTCTTTGCCC GGTCCACTGT GGTCCATCCG GACTCCAGAC ATCAGCCTCC CTTGACCCCT 3900
CGGCAACAGC CCCACCTGGA CTCTGGCTCC TTGTCCCCTG GACGGCAAGG CCAGCAGCCT 3960
CGAAGGGATC CCCCTAGAGA AGGCTTGCGG CCACCCCCCT ACAGACCGCG CAGAGACGCT 4020
TTTGAAATTT CTACTGAAGG GCATTCTGGC CCTAGCAATA GGGACCGCTC AGGGCCCCGT 4080
GGGGCCCGTT CTCACAACCC TCGGAACCCA ACGTCCACCG CCATGGGCAG CTCTGTGCCC 4140
AGCTACTGCC AGCCCATCAC CACTGTGACG GCTTCTGCTT CGGTGACTGT TGCTGTGCAT 4200
CCCCCGCCTG GACCTGGGCG CAACCCCCGA GGGGGGCCCT GTCCAGGCTA TGAGAGCTAC 4260
CCTGAGACTG ATCACGGGGT ATTTGAGGAT CCTCATGTGC CTTTTCATGT CAGGTGTGAG 4320
AGGAGGGACT CAAAGGTGGA GGTCATAGAG CTACAGGACG TGGAATGTGA GGAGAGGCCG 4380
TGGGGGAGCA GCTCCAACTG AGGGTAATTA AAATCTGAAG CAAAGAGGCC AAAGATTGGA 4440
AAGCCCCGCC CCCACCTCTT TCCAGAACTG CTTGAAGAGA ACTGCTTGGA ATTATGGGAA 4500
GGCAGTTCAT TGTTACTGTA ACTGATTGTA TTATTKKGTG AAATATTTCT ATAAATATTT 4560
AARAGGTGTA CACATGTAAT ATACATGGAA ATGCTGTACA GTCTATTTCC TGGGGCCTCT 4620
CCACTCCTGC CCCAGAGTGG GGAGACCACA GGGGCCCTTT CCCCTGTGTA CATTGGTCTC 4680
TGTGCCACAA CCAAGCTTAA CTTAGTTTTA AAAAAAATCT CCCAGCATAT GTCGCTGCTG 4740

CTTAAATATT GTATAATTTA CTTGTATAAT TCTATGCAAA TATTGCTTAT GTAATAGGAT 4800

TATTTGTAAA GGTTTCTGTT TAAAATATTT TAAATTTGCA TATCACAACC CTGTGGTAGG 4860

ATGAATTGTT ACTGTTAACT TTTGAACACG CTATGCGTGG TAATTGTTTA ACGAGCAGAC 4920

ATGAAGAAAA CAGGTTAATC CCAGTGGCTT CTCTAGGGGT AGTTGTATAT GGTTCGCATG 4980

GGTGGATGTG TGTGTGCATG TGACTTTCCA ATGTACTGTA TTGTGGTTTG TTGTTGTTGT 5040

TGCTGTTGTT GTTCATTTTG GTGTTTTTGG TTGCTTTGTA TGATCTTAGC TCTGGCCTAG 5100

GTGGGCTGGG AAGGTCCAGG TCTTTTTCTG TCGTGATGCT GGTGGAAAGG TGACCCCAAT 5160

CATCTGTCCT ATTCTCTGGG ACTATTC 5187

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Ala Pro Asp Ser Glu Ala Pro Ser Asn Pro Arg Ile Thr Ala
1 5 10 15

Ala His Glu Ser Pro Cys Ala Thr Glu Ala Arg His Ser Ala Asp Leu
20 25 30

Tyr Ile Arg Thr Ser Trp Val Asp Ala Ala Leu Ala Leu Ser Glu Leu
35 40 45

Glu Lys Gly Asn Ile Glu Gly Gly Arg Thr Ser Leu Trp Ile Arg Ala
50 55 60

Trp Leu Gln Glu Gln Leu Phe Ile Leu Gly Cys Phe Leu Gln Gly Asp
65 70 75 80

Ala Gly Lys Val Leu Phe Val Ala Ile Leu Val Leu Ser Thr Phe Cys
85 90 95

Val Gly Leu Lys Ser Ala Gln Ile His Thr Arg Val Asp Gln Leu Trp
100 105 110

Val Gln Glu Gly Gly Arg Leu Glu Ala Glu Leu Lys Tyr Thr Ala Gln
115 120 125

Ala Leu Gly Glu Ala Asp Ser Ser Thr His Gln Leu Val Ile Gln Thr
130 135 140

Ala Lys Asp Pro Asp Val Ser Leu Leu His Pro Gly Ala Leu Leu Glu
145 150 155 160

His Leu Lys Val Val His Ala Ala Thr Arg Val Thr Val His Met Tyr
165 170 175

Asp Ile Glu Trp Arg Leu Lys Asp Leu Cys Tyr Ser Pro Ser Ile Pro
180 185 190

Asp Phe Glu Gly Tyr His His Ile Glu Ser Ile Ile Asp Asn Val Ile
195 200 205

Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ser Lys
210 215 220

Leu Leu Gly Pro Asp Tyr Pro Ile Tyr Val Pro His Leu Lys His Lys
225 230 235 240

Leu Gln Trp Thr His Leu Asn Pro Leu Glu Val Val Glu Glu Val Lys
245 250 255

Lys Leu Lys Phe Gln Phe Pro Leu Ser Thr Ile Glu Ala Tyr Met Lys
260 265 270

Arg Ala Gly Ile Thr Ser Ala Tyr Met Lys Lys Pro Cys Leu Asp Pro
275 280 285

Thr Asp Pro His Cys Pro Ala Thr Ala Pro Asn Lys Lys Ser Gly His
290 295 300

Ile Pro Asp Val Ala Ala Glu Leu Ser His Gly Cys Tyr Gly Phe Ala
305 310 315 320

Ala Ala Tyr Met His Trp Pro Glu Gln Leu Ile Val Gly Gly Ala Thr
325 330 335

Arg Asn Ser Thr Ser Ala Leu Arg Lys Ala Arg Xaa Leu Gln Thr Val
340 345 350

Val Gln Leu Met Gly Glu Arg Glu Met Tyr Glu Tyr Trp Ala Asp His
355 360 365

Tyr Lys Val His Gln Ile Gly Trp Asn Gln Glu Lys Ala Ala Ala Val
370 375 380

Leu Asp Ala Trp Gln Arg Lys Phe Ala Ala Glu Val Arg Lys Ile Thr
385 390 395 400

Thr Ser Gly Ser Val Ser Ser Ala Tyr Ser Phe Tyr Pro Phe Ser Thr
405 410 415

Ser Thr Leu Asn Asp Ile Leu Gly Lys Phe Ser Glu Val Ser Leu Lys
420 425 430

Asn Ile Ile Leu Gly Tyr Met Phe Met Leu Ile Tyr Val Ala Val Thr
435 440 445

Leu Ile Gln Trp Arg Asp Pro Ile Arg Ser Gln Ala Gly Val Gly Ile

450 455 460

Ala Gly Val Leu Leu Leu Ser Ile Thr Val Ala Ala Gly Leu Gly Phe
465 470 475 480

Cys Ala Leu Leu Gly Ile Pro Phe Asn Ala Ser Ser Thr Gln Ile Val
485 490 495

Pro Phe Leu Ala Leu Gly Leu Gly Val Gln Asp Met Phe Leu Leu Thr
500 505 510

His Thr Tyr Val Glu Gln Ala Gly Asp Val Pro Arg Glu Glu Arg Thr
515 520 525

Gly Leu Val Leu Lys Lys Ser Gly Leu Ser Val Leu Leu Ala Ser Leu
530 535 540

Cys Asn Val Met Ala Phe Leu Ala Ala Ala Leu Leu Pro Ile Pro Ala
545 550 555 560

Phe Arg Val Phe Cys Leu Gln Ala Ala Ile Leu Leu Leu Phe Asn Leu
565 570 575

Gly Ser Ile Leu Leu Val Phe Pro Ala Met Ile Ser Leu Asp Leu Arg
580 585 590

Arg Arg Ser Ala Ala Arg Ala Asp Leu Leu Cys Cys Leu Met Pro Glu
595 600 605

Ser Pro Leu Pro Lys Lys Lys Ile Pro Glu Arg Ala Lys Thr Arg Lys
610 615 620

Asn Asp Lys Thr His Arg Ile Asp Thr Thr Arg Gln Pro Leu Asp Pro
625 630 635 640

Asp Val Ser Glu Asn Val Thr Lys Thr Cys Cys Leu Ser Val Ser Leu
645 650 655

Thr Lys Trp Ala Lys Asn Gln Tyr Ala Pro Phe Ile Met Arg Pro Ala
660 665 670

Val Lys Val Thr Ser Met Leu Ala Leu Ile Ala Val Ile Leu Thr Ser
675 680 685

Val Trp Gly Ala Thr Lys Val Lys Asp Gly Leu Asp Leu Thr Asp Ile
690 695 700

Val Pro Glu Asn Thr Asp Glu His Glu Phe Leu Ser Arg Gln Glu Lys
705 710 715 720

Tyr Phe Gly Phe Tyr Asn Met Tyr Ala Val Thr Gln Gly Asn Phe Glu
725 730 735

Tyr Pro Thr Asn Gln Lys Leu Leu Tyr Glu Tyr His Asp Gln Phe Val
740 745 750

Arg Ile Pro Asn Ile Ile Lys Asn Asp Asn Gly Gly Leu Thr Lys Phe
755 760 765

Trp Leu Ser Leu Phe Arg Asp Trp Leu Leu Asp Leu Gln Val Ala Phe
770 775 780

Asp Lys Glu Val Ala Ser Gly Cys Ile Thr Gln Glu Tyr Trp Cys Lys
785 790 795 800

Asn Ala Ser Asp Glu Gly Ile Leu Ala Tyr Lys Leu Met Val Gln Thr
805 810 815

Gly His Val Asp Asn Pro Ile Asp Lys Ser Leu Ile Thr Ala Gly His
820 825 830

Arg Leu Val Asp Lys Asp Gly Ile Ile Asn Pro Lys Ala Phe Tyr Asn
835 840 845

Tyr Leu Ser Ala Trp Ala Thr Asn Asp Ala Leu Ala Tyr Gly Ala Ser
850 855 860

Gln Gly Asn Leu Lys Pro Gln Pro Gln Arg Trp Ile His Ser Pro Glu
865 870 875 880

Asp Val His Leu Glu Ile Lys Lys Ser Ser Pro Leu Ile Tyr Thr Gln
885 890 895

Leu Pro Phe Tyr Leu Ser Gly Leu Ser Asp Thr Xaa Ser Ile Lys Thr
900 905 910

Leu Ile Arg Ser Val Arg Asp Leu Cys Leu Lys Tyr Glu Ala Lys Gly
915 920 925

Leu Pro Asn Phe Pro Ser Gly Ile Pro Phe Leu Phe Trp Glu Gln Tyr
930 935 940

Leu Tyr Leu Arg Thr Ser Leu Leu Leu Ala Leu Ala Cys Ala Leu Ala
945 950 955 960

Ala Val Phe Ile Ala Val Met Val Leu Leu Leu Asn Ala Trp Ala Ala
965 970 975

Val Leu Val Thr Leu Ala Leu Ala Thr Leu Val Leu Gln Leu Leu Gly
980 985 990

Val Met Ala Leu Leu Gly Val Lys Leu Ser Ala Met Pro Ala Val Leu
995 1000 1005

Leu Val Leu Ala Ile Gly Arg Gly Val His Phe Thr Val His Leu Cys
1010 1015 1020

Leu Gly Phe Val Thr Ser Ile Gly Cys Lys Arg Arg Arg Ala Ser Leu
1025 1030 1035 1040

Ala Leu Glu Ser Val Leu Ala Pro Val Val His Gly Ala Leu Ala Ala
1045 1050 1055

Ala Leu Ala Ala Ser Met Leu Ala Ala Ser Glu Cys Gly Phe Val Ala
1060 1065 1070

Arg Leu Phe Leu Arg Leu Leu Leu Asp Ile Val Phe Leu Gly Leu Ile

1075 1080 1085

Asp Gly Leu Leu Phe Phe Pro Ile Val Leu Ser Ile Leu Gly Pro Ala
1090 1095 1100

Ala Glu Val Arg Pro Ile Glu His Pro Glu Arg Leu Ser Thr Pro Ser
1105 1110 1115 1120

Pro Lys Cys Ser Pro Ile His Pro Arg Lys Ser Ser Ser Ser Ser Gly
1125 1130 1135

Gly Gly Asp Lys Ser Ser Arg Thr Ser Lys Ser Ala Pro Arg Pro Cys
1140 1145 1150

Ala Pro Ser Leu Thr Thr Ile Thr Glu Glu Pro Ser Ser Trp His Ser
1155 1160 1165

Ser Ala His Ser Val Gln Ser Ser Met Gln Ser Ile Val Val Gln Pro
1170 1175 1180

Glu Val Val Val Glu Thr Thr Thr Tyr Asn Gly Ser Asp Ser Ala Ser
1185 1190 1195 1200

Gly Arg Ser Thr Pro Thr Lys Ser Ser His Gly Gly Ala Ile Thr Thr
1205 1210 1215

Thr Lys Val Thr Ala Thr Ala Asn Ile Lys Val Glu Val Val Thr Pro
1220 1225 1230

Ser Asp Arg Lys Ser Arg Arg Ser Tyr His Tyr Tyr Asp Arg Arg Arg
1235 1240 1245

Asp Arg Asp Glu Asp Arg Asp Arg Asp Arg Glu Arg Asp Arg Asp Arg
1250 1255 1260

Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg Asp Arg
1265 1270 1275 1280

Glu Arg Ser Arg Glu Arg Asp Arg Arg Asp Arg Tyr Arg Asp Glu Arg
1285 1290 1295

Asp His Arg Ala Ser Pro Arg Glu Lys Arg Gln Arg Phe Trp Thr
1300 1305 1310

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 4434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAACAAGA GAGCGAGTGA GAGTAGGGAG AGCGTCTGTG TTGTGTGTTG AGTGTCGCCC 60

ACGCACACAG GCGCAAAACA GTGCACACAG ACGCCCGCTG GGCAAGAGAG AGTGAGAGAG 120

AGAAACAGCG GCGCGCGCTC GCCTAATGAA GTTGTTGGCC TGGCTGGCGT GCCGCATCCA 180

CGAGATACAG ATACATCTCT CATGGACCGC GACAGCCTCC CACGCGTTCC GGACACACAC 240

GGCGATGTGG TCGATGAGAA ATTATTCTCG GATCTTTACA TACGCACCAG CTGGGTGGAC 300

GCCCAAGTGG CGCTCGATCA GATAGATAAG GGCAAAGCGC GTGGCAGCCG CACGGCGATC 360

TATCTGCGAT CAGTATTCCA GTCCCACCTC GAAACCCTCG GCAGCTCCGT GCAAAAGCAC 420

GCGGGCAAGG TGCTATTCGT GGCTATCCTG GTGCTGAGCA CCTTCTGCGT CGGCCTGAAG 480

AGCGCCCAGA TCCACTCCAA GGTGCACCAG CTGTGGATCC AGGAGGGCGG CCGGCTGGAG 540

GCGGAACTGG CCTACACACA GAAGACGATC GGCGAGGACG AGTCGGCCAC GCATCAGCTG 600

CTCATTCAGA CGACCCACGA CCCGAACGCC TCCGTCCTGC ATCCGCAGGC GCTGCTTGCC 660

CACCTGGAGG TCCTGGTCAA GGCCACCGCC GTCAAGGTGC ACCTCTACGA CACCGAATGG 720

GGGCTGCGCG ACATGTGCAA CATGCCGAGC ACGCCCTCCT TCGAGGGCAT CTACTACATC 780

GAGCAGATCC TGCGCCACCT CATTCCGTGC TCGATCATCA CGCCGCTGGA CTGTTTCTGG 840

GAGGGAAGCC AGCTGTTGGG TCCGGAATCA GCGGTCGTTA TACCAGGCCT CAACCAACGA 900

CTCCTGTGGA CCACCCTGAA TCCCGCCTCT GTGATGCAGT ATATGAAACA AAAGATGTCC 960

GAGGAAAAGA TCAGCTTCGA CTTCGAGACC GTGGAGCAGT ACATGAAGCG TGCGGCCATT 1020

GGCAGTGGCT ACATGGAGAA GCCCTGCCTG AACCCACTGA ATCCCAATTG CCCGGACACG 1080

GCACCGAACA AGAACAGCAC CCAGCCGCCG GATGTGGGAG CCATCCTGTC CGGAGGCTGC 1140

TACGGTTATG CCGCGAAGCA CATGCACTGG CCGGAGGAGC TGATTGTGGG CGGACGGAAG 1200

AGGAACCGCA GCGGACACTT GAGGAAGGCC CAGGCCCTGC AGTCGGTGGT GCAGCTGATG 1260

ACCGAGAAGG AAATGTACGA CCAGTGGCAG GACAACTACA AGGTGCACCA TCTTGGATGG 1320

ACGCAGGAGA AGGCAGCGGA GGTTTTGAAC GCCTGGCAGC GCAACTTTTC GCGGGAGGTG 1380

GAACAGCTGC TACGTAAACA GTCGAGAATT GCCACCAACT ACGATATCTA CGTGTTCAGC 1440

TCGGCTGCAC TGGATGACAT CCTGGCCAAG TTCTCCCATC CCAGCGCCTT GTCCATTGTC 1500

ATCGGCGTGG CCGTCACCGT TTTGTATGCC TTTTGCACGC TCCTCCGCTG GAGGGACCCC 1560

GTCCGTGGCC AGAGCAGTGT GGGCGTGGCC GGAGTTCTGC TCATGTGCTT CAGTACCGCC 1620

GCCGGATTGG GATTGTCAGC CCTGCTCGGT ATCGTTTTCA ATGCGCTGAC CGCTGCCTAT 1680

GCGGAGAGCA ATCGGCGGGA GCAGACCAAG CTGATTCTCA AGAACGCCAG CACCCAGGTG 1740

GTTCCGTTTT TGGCCCTTGG TCTGGGCGTC GATCACATCT TCATAGTGGG ACCGAGCATC 1800

CTGTTCAGTG CCTGCAGCAC CGCAGGATCC TTCTTTGCGG CCGCCTTTAT TCCGGTGCCG 1860

GCTTTGAAGG TATTCTGTCT GCAGGCTGCC ATCGTAATGT GCTCCAATTT GGCAGCGGCT 1920

CTATTGGTTT TTCCGGCCAT GATTTCGTTG GATCTACGGA GACGTACCGC CGGCAGGGCG 1980

GACATCTTCT GCTGCTGTTT TCCGGTGTGG AAGGAACAGC CGAAGGTGGC ACCTCCGGTG 2040

CTGCCGCTGA ACAACAACAA CGGGCGCGGG GCCCGGCATC CGAAGAGCTG CAACAACAAC 2100

AGGGTGCCGC TGCCCGCCCA GAATCCTCTG CTGGAACAGA GGGCAGACAT CCCTGGGAGC 2160

AGTCACTCAC TGGCGTCCTT CTCCCTGGCA ACCTTCGCCT TTCAGCACTA CACTCCCTTC 2220

CTCATGCGCA GCTGGGTGAA GTTCCTGACC GTTATGGGTT TCCTGGCGGC CCTCATATCC 2280

AGCTTGTATG CCTCCACGCG CCTTCAGGAT GGCCTGGACA TTATTGATCT GGTGCCCAAG 2340

GACAGCAACG AGCACAAGTT CCTGGATGCT CAAACTCGGC TCTTTGGCTT CTACAGCATG 2400

TATGCGGTTA CCCAGGGCAA CTTTGAATAT CCCACCCAGC AGCAGTTGCT CAGGGACTAC 2460

CATGATTCCT TTGTGCGGGT GCCACATGTG ATCAAGAATG ATAACGGTGG ACTGCCGGAC 2520

TTCTGGCTGC TGCTCTTCAG CGAGTGGCTG GGTAATCTGC AAAAGATATT CGACGAGGAA 2580

TACCGCGACG GACGGCTGAC CAAGGAGTGC TGGTTCCCAA ACGCCAGCAG CGATGCCATC 2640

CTGGCCTACA AGCTAATCGT GCAAACCGGC CATGTGGACA ACCCCGTGGA CAAGGAACTG 2700

GTGCTCACCA ATCGCCTGGT CAACAGCGAT GGCATCATCA ACCAACGCGC CTTCTACAAC 2760

TATCTGTCGG CATGGGCCAC CAACGACGTC TTCGCCTACG GAGCTTCTCA GGGCAAATTG 2820

TATCCGGAAC CGCGCCAGTA TTTTCACCAA CCCAACGAGT ACGATCTTAA GATACCCAAG 2880

AGTCTGCCAT TGGTCTACGC TCAGATGCCC TTTTACCTCC ACGGACTAAC AGATACCTCG 2940

CAGATCAAGA CCCTGATAGG TCATATTCGC GACCTGAGCG TCAAGTACGA GGGCTTCGGC 3000

CTGCCCAACT ATCCATCGGG CATTCCCTTC ATCTTCTGGG AGCAGTACAT GACCCTGCGC 3060

TCCTCACTGG CCATGATCCT GGCCTGCGTG CTACTCGCCG CCCTGGTGCT GGTCTCCCTG 3120

CTCCTGCTCT CCGTTTGGGC CGCCGTTCTC GTGATCCTCA GCGTTCTGGC CTCGCTGGCC 3180

CAGATCTTTG GGGCCATGAC TCTGCTGGGC ATCAAACTCT CGGCCATTCC GGCAGTCATA 3240

CTCATCCTCA GCGTGGGCAT GATGCTGTGC TTCAATGTGC TGATATCACT GGGCTTCATG 3300

ACATCCGTTG GCAACCGACA GCGCCGCGTC CAGCTGAGCA TGCAGATGTC CCTGGGACCA 3360

CTTGTCCACG GCATGCTGAC CTCCGGAGTG GCCGTGTTCA TGCTCTCCAC GTCGCCCTTT 3420

GAGTTTGTGA TCCGGCACTT CTGCTGGCTT CTGCTGGTGG TCTTATGCGT TGGCGCCTGC 3480

AACAGCCTTT TGGTGTTCCC CATCCTACTG AGCATGGTGG GACCGGAGGC GGAGCTGGTG 3540

CCGCTGGAGC ATCCAGACCG CATATCCACG CCCTCTCCGC TGCCCGTGCG CAGCAGCAAG 3600

AGATCGGGCA AATCCTATGT GGTGCAGGGA TCGCGATCCT CGCGAGGCAG CTGCCAGAAG 3660

TCGCATCACC ACCACCACAA AGACCTTAAT GATCCATCGC TGACGACGAT CACCGAGGAG 3720

CCGCAGTCGT GGAAGTCCAG CAACTCGTCC ATCCAGATGC CCAATGATTG GACCTACCAG 3780

CCGCGGGAAC AGCGACCCGC CTCCTACGCG GCCCCGCCCC CCGCCTATCA CAAGGCCGCC 3840

GCCCAGCAGC ACCACCAGCA TCAGGGCCCG CCCACAACGC CCCCGCCTCC CTTCCCGACG 3900

GCCTATCCGC CGGAGCTGCA GAGCATCGTG GTGCAGCCGG AGGTGACGGT GGAGACGACG 3960

CACTCGGACA GCAACACCAC CAAGGTGACG GCCACGGCCA ACATCAAGGT GGAGCTGGCC 4020

ATGCCCGGCA GGGCGGTGCG CAGCTATAAC TTTACGAGTT AGCACTAGCA CTAGTTCCTG 4080

TAGCTATTAG GACGTATCTT TAGACTCTAG CCTAAGCCGT AACCCTATTT GTATCTGTAA 4140

AATCGATTTG TCCAGCGGGT CTGCTGAGGA TTTCGTTCTC ATGGATTCTC ATGGATTCTC 4200

ATGGATGCTT AAATGGCATG GTAATTGGCA AAATATCAAT TTTTGTGTCT CAAAAAGATG 4260

CATTAGCTTA TGGTTTCAAG ATACATTTTT AAAGAGTCCG CCAGATATTT ATATAAAAAA 4320

AATCCAAAAT CGACGTATCC ATGAAAATTG AAAAGCTAAG CAGACCCGTA TGTATGTATA 4380

TGTGTATGCA TGTTAGTTAA TTTCCCGAAG TCCGGTATTT ATAGCAGCTG CCTT 4434

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1285 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Asp Arg Asp Ser Leu Pro Arg Val Pro Asp Thr His Gly Asp Val
1 5 10 15

Val Asp Glu Lys Leu Phe Ser Asp Leu Tyr Ile Arg Thr Ser Trp Val
20 25 30

Asp Ala Gln Val Ala Leu Asp Gln Ile Asp Lys Gly Lys Ala Arg Gly
35 40 45

Ser Arg Thr Ala Ile Tyr Leu Arg Ser Val Phe Gln Ser His Leu Glu
50 55 60

Thr Leu Gly Ser Ser Val Gln Lys His Ala Gly Lys Val Leu Phe Val
65 70 75 80

Ala Ile Leu Val Leu Ser Thr Phe Cys Val Gly Leu Lys Ser Ala Gln
85 90 95

Ile His Ser Lys Val His Gln Leu Trp Ile Gln Glu Gly Gly Arg Leu
100 105 110

Glu Ala Glu Leu Ala Tyr Thr Gln Lys Thr Ile Gly Glu Asp Glu Ser
115 120 125

Ala Thr His Gln Leu Leu Ile Gln Thr Thr His Asp Pro Asn Ala Ser
130 135 140

Val Leu His Pro Gln Ala Leu Leu Ala His Leu Glu Val Leu Val Lys
145 150 155 160

Ala Thr Ala Val Lys Val His Leu Tyr Asp Thr Glu Trp Gly Leu Arg
165 170 175

Asp Met Cys Asn Met Pro Ser Thr Pro Ser Phe Glu Gly Ile Tyr Tyr
180 185 190

Ile Glu Gln Ile Leu Arg His Leu Ile Pro Cys Ser Ile Ile Thr Pro
195 200 205

Leu Asp Cys Phe Trp Glu Gly Ser Gln Leu Leu Gly Pro Glu Ser Ala
210 215 220

Val Val Ile Pro Gly Leu Asn Gln Arg Leu Leu Trp Thr Thr Leu Asn
225 230 235 240

Pro Ala Ser Val Met Gln Tyr Met Lys Gln Lys Met Ser Glu Glu Lys
245 250 255

Ile Ser Phe Asp Phe Glu Thr Val Glu Gln Tyr Met Lys Arg Ala Ala
260 265 270

Ile Gly Ser Gly Tyr Met Glu Lys Pro Cys Leu Asn Pro Leu Asn Pro
275 280 285

Asn Cys Pro Asp Thr Ala Pro Asn Lys Asn Ser Thr Gln Pro Pro Asp
290 295 300

Val Gly Ala Ile Leu Ser Gly Gly Cys Tyr Gly Tyr Ala Ala Lys His
305 310 315 320

Met His Trp Pro Glu Glu Leu Ile Val Gly Gly Arg Lys Arg Asn Arg
325 330 335

Ser Gly His Leu Arg Lys Ala Gln Ala Leu Gln Ser Val Val Gln Leu
340 345 350

Met Thr Glu Lys Glu Met Tyr Asp Gln Trp Gln Asp Asn Tyr Lys Val
355 360 365

His His Leu Gly Trp Thr Gln Glu Lys Ala Ala Glu Val Leu Asn Ala

370 375 380

Trp Gln Arg Asn Phe Ser Arg Glu Val Glu Gln Leu Leu Arg Lys Gln
385 390 395 400

Ser Arg Ile Ala Thr Asn Tyr Asp Ile Tyr Val Phe Ser Ser Ala Ala
405 410 415

Leu Asp Asp Ile Leu Ala Lys Phe Ser His Pro Ser Ala Leu Ser Ile
420 425 430

Val Ile Gly Val Ala Val Thr Val Leu Tyr Ala Phe Cys Thr Leu Leu
435 440 445

Arg Trp Arg Asp Pro Val Arg Gly Gln Ser Ser Val Gly Val Ala Gly
450 455 460

Val Leu Leu Met Cys Phe Ser Thr Ala Ala Gly Leu Gly Leu Ser Ala
465 470 475 480

Leu Leu Gly Ile Val Phe Asn Ala Leu Thr Ala Ala Tyr Ala Glu Ser
485 490 495

Asn Arg Arg Glu Gln Thr Lys Leu Ile Leu Lys Asn Ala Ser Thr Gln
500 505 510

Val Val Pro Phe Leu Ala Leu Gly Leu Gly Val Asp His Ile Phe Ile
515 520 525

Val Gly Pro Ser Ile Leu Phe Ser Ala Cys Ser Thr Ala Gly Ser Phe
530 535 540

Phe Ala Ala Ala Phe Ile Pro Val Pro Ala Leu Lys Val Phe Cys Leu
545 550 555 560

Gln Ala Ala Ile Val Met Cys Ser Asn Leu Ala Ala Ala Leu Leu Val
565 570 575

Phe Pro Ala Met Ile Ser Leu Asp Leu Arg Arg Arg Thr Ala Gly Arg
580 585 590

Ala Asp Ile Phe Cys Cys Cys Phe Pro Val Trp Lys Glu Gln Pro Lys
595 600 605

Val Ala Pro Pro Val Leu Pro Leu Asn Asn Asn Asn Gly Arg Gly Ala
610 615 620

Arg His Pro Lys Ser Cys Asn Asn Asn Arg Val Pro Leu Pro Ala Gln
625 630 635 640

Asn Pro Leu Leu Glu Gln Arg Ala Asp Ile Pro Gly Ser Ser His Ser
645 650 655

Leu Ala Ser Phe Ser Leu Ala Thr Phe Ala Phe Gln His Tyr Thr Pro
660 665 670

Phe Leu Met Arg Ser Trp Val Lys Phe Leu Thr Val Met Gly Phe Leu
675 680 685

Ala Ala Leu Ile Ser Ser Leu Tyr Ala Ser Thr Arg Leu Gln Asp Gly
690 695 700

Leu Asp Ile Ile Asp Leu Val Pro Lys Asp Ser Asn Glu His Lys Phe
705 710 715 720

Leu Asp Ala Gln Thr Arg Leu Phe Gly Phe Tyr Ser Met Tyr Ala Val
725 730 735

Thr Gln Gly Asn Phe Glu Tyr Pro Thr Gln Gln Gln Leu Leu Arg Asp
740 745 750

Tyr His Asp Ser Phe Arg Val Pro His Val Ile Lys Asn Asp Asn Gly
755 760 765

Gly Leu Pro Asp Phe Trp Leu Leu Leu Phe Ser Glu Trp Leu Gly Asn
770 775 780

Leu Gln Lys Ile Phe Asp Glu Glu Tyr Arg Asp Gly Arg Leu Thr Lys
785 790 795 800

Glu Cys Trp Phe Pro Asn Ala Ser Ser Asp Ala Ile Leu Ala Tyr Lys
805 810 815

Leu Ile Val Gln Thr Gly His Val Asp Asn Pro Val Asp Lys Glu Leu
820 825 830

Val Leu Thr Asn Arg Leu Val Asn Ser Asp Gly Ile Ile Asn Gln Arg
835 840 845

Ala Phe Tyr Asn Tyr Leu Ser Ala Trp Ala Thr Asn Asp Val Phe Ala
850 855 860

Tyr Gly Ala Ser Gln Gly Lys Leu Tyr Pro Glu Pro Arg Gln Tyr Phe
865 870 875 880

His Gln Pro Asn Glu Tyr Asp Leu Lys Ile Pro Lys Ser Leu Pro Leu
885 890 895

Val Tyr Ala Gln Met Pro Phe Tyr Leu His Gly Leu Thr Asp Thr Ser
900 905 910

Gln Ile Lys Thr Leu Ile Gly His Ile Arg Asp Leu Ser Val Lys Tyr
915 920 925

Glu Gly Phe Gly Leu Pro Asn Tyr Pro Ser Gly Ile Pro Phe Ile Phe
930 935 940

Trp Glu Gln Tyr Met Thr Leu Arg Ser Ser Leu Ala Met Ile Leu Ala
945 950 955 960

Cys Val Leu Leu Ala Ala Leu Val Leu Val Ser Leu Leu Leu Leu Ser
965 970 975

Val Trp Ala Ala Val Leu Val Ile Leu Ser Val Leu Ala Ser Leu Ala
980 985 990

Gln Ile Phe Gly Ala Met Thr Leu Leu Gly Ile Lys Leu Ser Ala Ile

995 1000 1005

Pro Ala Val Ile Leu Ile Leu Ser Val Gly Met Met Leu Cys Phe Asn
1010 1015 1020

Val Leu Ile Ser Leu Gly Phe Met Thr Ser Val Gly Asn Arg Gln Arg
1025 1030 1035 1040

Arg Val Gln Leu Ser Met Gln Met Ser Leu Gly Pro Leu Val His Gly
1045 1050 1055

Met Leu Thr Ser Gly Val Ala Val Phe Met Leu Ser Thr Ser Pro Phe
1060 1065 1070

Glu Phe Val Ile Arg His Phe Cys Trp Leu Leu Leu Val Val Leu Cys
1075 1080 1085

Val Gly Ala Cys Asn Ser Leu Leu Val Phe Pro Ile Leu Leu Ser Met
1090 1095 1100

Val Gly Pro Glu Ala Glu Leu Val Pro Leu Glu His Pro Asp Arg Ile
1105 1110 1115 1120

Ser Thr Pro Ser Pro Leu Pro Val Arg Ser Ser Lys Arg Ser Gly Lys
1125 1130 1135

Ser Tyr Val Val Gln Gly Ser Arg Ser Ser Arg Gly Ser Cys Gln Lys
1140 1145 1150

Ser His His His His His Lys Asp Leu Asn Asp Pro Ser Leu Thr Thr
1155 1160 1165

Ile Thr Glu Glu Pro Gln Ser Trp Lys Ser Ser Asn Ser Ser Ile Gln
1170 1175 1180

Met Pro Asn Asp Trp Thr Tyr Gln Pro Arg Glu Gln Arg Pro Ala Ser
1185 1190 1195 1200

Tyr Ala Ala Pro Pro Pro Ala Tyr His Lys Ala Ala Ala Gln Gln His
1205 1210 1215

His Gln His Gln Gly Pro Pro Thr Thr Pro Pro Pro Pro Phe Pro Thr
1220 1225 1230

Ala Tyr Pro Pro Glu Leu Gln Ser Ile Val Val Gln Pro Glu Val Thr
1235 1240 1245

Val Glu Thr Thr His Ser Asp Ser Asn Thr Thr Lys Val Thr Ala Thr
1250 1255 1260

Ala Asn Ile Lys Val Glu Leu Ala Met Pro Gly Arg Ala Val Arg Ser
1265 1270 1275 1280

Tyr Asn Phe Thr Ser
1285

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 345 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGGTCCATC AGCTTTGGAT ACAGGAAGGT GGTTCGCTCG AGCATGAGCT AGCCTACACG 60

CAGAAATCGC TCGGCGAGAT GGACTCCTCC ACGCACCAGC TGCTAATCCA AACNCCCAAA 120

GATATGGACG CCTCGATACT GCACCCGAAC GCGCTACTGA CGCACCTGGA CGTGGTGAAG 180

AAAGCGATCT CGGTGACGGT GCACATGTAC GACATCACGT GGAGNCTCAA GGACATGTGC 240

TACTCGCCCA GCATACCGAG NTTCGATACG CACTTTATCG AGCAGATCTT CGAGAACATC 300

ATACCGTGCG CGATCATCAC GCCGCTGGAT TGCTTTTGGG AGGGA 345

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 115 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Val His Gln Leu Trp Ile Gln Glu Gly Gly Ser Leu Glu His Glu
1 5 10 15

Leu Ala Tyr Thr Gln Lys Ser Leu Gly Glu Met Asp Ser Ser Thr His
20 25 30

Gln Leu Leu Ile Gln Thr Pro Lys Asp Met Asp Ala Ser Ile Leu His
35 40 45

Pro Asn Ala Leu Leu Thr His Leu Asp Val Val Lys Lys Ala Ile Ser
50 55 60

Val Thr Val His Met Tyr Asp Ile Thr Trp Xaa Leu Lys Asp Met Cys
65 70 75 80

Tyr Ser Pro Ser Ile Pro Xaa Phe Asp Thr His Phe Ile Glu Gln Ile
85 90 95

Phe Glu Asn Ile Ile Pro Cys Ala Ile Ile Thr Pro Leu Asp Cys Phe
100 105 110

Trp Glu Gly
115

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5187 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GGGTCTGTCA CCCGGAGCCG GAGTCCCCGG CGGCCAGCAG CGTCCTCGCG AGCCGAGCGC 60

CCAGGCGCGC CCGGAGCCCG CGGCGGCGGC GGCAACATGG CCTCGGCTGG TAACGCCGCC 120

GGGGCCCTGG GCAGGCAGGC CGGCGGCGGG AGGCGCAGAC GGACCGGGGG ACCGCACCGC 180

GCCGCGCCGG ACCGGGACTA TCTGCACCGG CCCAGCTACT GCGACGCCGC CTTCGCTCTG 240

GAGCAGATTT CCAAGGGGAA GGCTACTGGC CGGAAAGCGC CGCTGTGGCT GAGAGCGAAG 300

TTTCAGAGAC TCTTATTTAA ACTGGGTTGT TACATTCAAA AGAACTGCGG CAAGTTTTTG 360

GTTGTGGGTC TCCTCATATT TGGGGCCTTC GCTGTGGGAT TAAAGGCAGC TAATCTCGAG 420

ACCAACGTGG AGGAGCTGTG GGTGGAAGTT GGTGGACGAG TGAGTCGAGA ATTAAATTAT 480

ACCCGTCAGA AGATAGGAGA AGAGGCTATG TTTAATCCTC AACTCATGAT ACAGACTCCA 540

AAAGAAGAAG GCGCTAATGT TCTGACCACA GAGGCTCTCC TGCAACACCT GGACTCAGCA 600

CTCCAGGCCA GTCGTGTGCA CGTCTACATG TATAACAGGC AATGGAAGTT GGAACATTTG 660

TGCTACAAAT CAGGGGAACT TATCACGGAG ACAGGTTACA TGGATCAGAT AATAGAATAC 720

CTTTACCCTT GCTTAATCAT TACACCTTTG GACTGCTTCT GGGAAGGGGC AAAGCTACAG 780

TCCGGGACAG CATACCTCCT AGGTAAGCCT CCTTTACGGT GGACAAACTT TGACCCCTTG 840

GAATTCCTAG AAGAGTTAAA GAAAATAAAC TACCAAGTGG ACAGCTGGGA GGAAATGCTG 900

AATAAAGCCG AAGTTGGCCA TGGGTACATG GACCGGCCTT GCCTCAACCC AGCCGACCCA 960

GATTGCCCTG CCACAGCCCC TAACAAAAAT TCAACCAAAC CTCTTGATGT GGCCCTTGTT 1020

TTGAATGGTG GATGTCAAGG TTTATCCAGG AAGTATATGC ATTGGCAGGA GGAGTTGATT 1080

GTGGGTGGTA CCGTCAAGAA TGCCACTGGA AAACTTGTCA GCGCTCACGC CCTGCAAACC 1140

ATGTTCCAGT TAATGACTCC CAAGCAAATG TATGAACACT TCAGGGGCTA CGACTATGTC 1200
TCTCACATCA ACTGGAATGA AGACAGGGCA GCCGCCATCC TGGAGGCCTG GCAGAGGACT 1260
TACGTGGAGG TGGTTCATCA AAGTGTCGCC CCAAACTCCA CTCAAAAGGT GCTTCCCTTC 1320
ACAACCACGA CCCTGGACGA CATCCTAAAA TCCTTCTCTG ATGTCAGTGT CATCCGAGTG 1380
GCCAGCGGCT ACCTACTGAT GCTTGCCTAT GCCTGTTTAA CCATGCTGCG CTGGGACTGC 1440
TCCAAGTCCC AGGGTGCCGT GGGGCTGGCT GGCGTCCTGT TGGTTGCGCT GTCAGTGGCT 1500
GCAGGATTGG GCCTCTGCTC CTTGATTGGC ATTTCTTTTA ATGCTGCGAC AACTCAGGTT 1560
TTGCCGTTTC TTGCTCTTGG TGTTGGTGTG GATGATGTCT TCCTCCTGGC CCATGCATTC 1620
AGTGAAACAG GACAGAATAA GAGGATTCCA TTTGAGGACA GGACTGGGGA GTGCCTCAAG 1680
CGCACCGGAG CCAGCGTGGC CCTCACCTCC ATCAGCAATG TCACCGCCTT CTTCATGGCC 1740
GCATTGATCC CTATCCCTGC CCTGCGAGCG TTCTCCCTCC AGGCTGCTGT GGTGGTGGTA 1800
TTCAATTTTG CTATGGTTCT GCTCATTTTT CCTGCAATTC TCAGCATGGA TTTATACAGA 1860
CGTGAGGACA GAAGATTGGA TATTTTCTGC TGTTTCACAA GCCCCTGTGT CAGCAGGGTG 1920
ATTCAAGTTG AGCCACAGGC CTACACAGAG CCTCACAGTA ACACCCGGTA CAGCCCCCCA 1980
CCCCCATACA CCAGCCACAG CTTCGCCCAC GAAACCCATA TCACTATGCA GTCCACCGTT 2040
CAGCTCCGCA CAGAGTATGA CCCTCACACG CACGTGTACT ACACCACCGC CGAGCCACGC 2100
TCTGAGATCT CTGTACAGCC TGTTACCGTC ACCCAGGACA ACCTCAGCTG TCAGAGTCCC 2160
GAGAGCACCA GCTCTACCAG GGACCTGCTC TCCCAGTTCT CAGACTCCAG CCTCCACTGC 2220
CTCGAGCCCC CCTGCACCAA GTGGACACTC TCTTCGTTTG CAGAGAAGCA CTATGCTCCT 2280
TTCCTCCTGA AACCCAAAGC CAAGGTTGTG GTAATCCTTC TTTTCCTGGG CTTGCTGGGG 2340
GTCAGCCTTT ATGGGACCAC CCGAGTGAGA GACGGGCTGG ACCTCACGGA CATTGTTCCC 2400
CGGGAAACCA GAGAATATGA CTTCATAGCT GCCCAGTTCA AGTACTTCTC TTTCTACAAC 2460
ATGTATATAG TCACCCAGAA AGCAGACTAC CCGAATATCC AGCACCTACT TTACGACCTT 2520
CATAAGAGTT TCAGCAATGT GAAGTATGTC ATGCTGGAGG AGAACAAGCA ACTTCCCCAA 2580
ATGTGGCTGC ACTACTTTAG AGACTGGCTT CAAGGACTTC AGGATGCATT TGACAGTGAC 2640
TGGGAAACTG GGAGGATCAT GCCAAACAAT TATAAAAATG GATCAGATGA CGGGGTCCTC 2700
GCTTACAAAC TCCTGGTGCA GACTGGCAGC CGAGACAAGC CCATCGACAT TAGTCAGTTG 2760
ACTAAACAGC GTCTGGTAGA CGCAGATGGC ATCATTAATC CGAGCGCTTT CTACATCTAC 2820
CTGACCGCTT GGGTCAGCAA CGACCCTGTA GCTTACGCTG CCTCCCAGGC CAACATCCGG 2880

CCTCACCGGC CGGAGTGGGT CCATGACAAA GCCGACTACA TGCCAGAGAC CAGGCTGAGA 2940
ATCCCAGCAG CAGAGCCCAT CGAGTACGCT CAGTTCCCTT TCTACCTCAA CGGCCTACGA 3000
GACACCTCAG ACTTTGTGGA AGCCATAGAA AAAGTGAGAG TCATCTGTAA CAACTATACG 3060
AGCCTGGGAC TGTCCAGCTA CCCCAATGGC TACCCCTTCC TGTTCTGGGA GCAATACATC 3120
AGCCTGCGCC ACTGGCTGCT GCTATCCATC AGCGTGGTGC TGGCCTGCAC GTTTCTAGTG 3180
TGCGCAGTCT TCCTCCTGAA CCCCTGGACG GCCGGGATCA TTGTCATGGT CCTGGCTCTG 3240
ATGACCGTTG AGCTCTTTGG CATGATGGGC CTCATTGGGA TCAAGCTGAG TGCTGTGCCT 3300
GTGGTCATCC TGATTGCATC TGTTGGCATC GGAGTGGAGT TCACCGTCCA CGTGGCTTTG 3360
GCCTTTCTGA CAGCCATTGG GGACAAGAAC CACAGGGCTA TGCTCGCTCT GGAACACATG 3420
TTTGCTCCCG TTCTGGACGG TGCTGTGTCC ACTCTGCTGG GTGTACTGAT GCTTGCAGGG 3480
TCCGAATTTG ATTTCATTGT CAGATACTTC TTTGCCGTCC TGGCCATTCT CACCGTCTTG 3540
GGGGTTCTCA ATGGACTGGT TCTGCTGCCT GTCCTCTTAT CCTTCTTTGG ACCGTGTCCT 3600
GAGGTGTCTC CAGCCAATGG CCTAAACCGA CTGCCCACTC CTTCGCCTGA GCCGCCTCCA 3660
AGTGTCGTCC GGTTTGCCGT GCCTCCTGGT CACACGAACA ATGGGTCTGA TTCCTCCGAC 3720
TCGGAGTACA GCTCTCAGAC CACGGTGTCT GGCATCAGTG AGGAGCTCAG GCAATACGAA 3780
GCACAGCAGG GTGCCGGAGG CCCTGCCCAC CAAGTGATTG TGGAAGCCAC AGAAAACCCT 3840
GTCTTTGCCC GGTCCACTGT GGTCCATCCG GACTCCAGAC ATCAGCCTCC CTTGACCCCT 3900
CGGCAACAGC CCCACCTGGA CTCTGGCTCC TTGTCCCCTG GACGGCAAGG CCAGCAGCCT 3960
CGAAGGGATC CCCCTAGAGA AGGCTTGCGG CCACCCCCCT ACAGACCGCG CAGAGACGCT 4020
TTTGAAATTT CTACTGAAGG GCATTCTGGC CCTAGCAATA GGGACCGCTC AGGGCCCCGT 4080
GGGGCCCGTT CTCACAACCC TCGGAACCCA ACGTCCACCG CCATGGGCAG CTCTGTGCCC 4140
AGCTACTGCC AGCCCATCAC CACTGTGACG GCTTCTGCTT CGGTGACTGT TGCTGTGCAT 4200
CCCCCGCCTG GACCTGGGCG CAACCCCCGA GGGGGGCCCT GTCCAGGCTA TGAGAGCTAC 4260
CCTGAGACTG ATCACGGGGT ATTTGAGGAT CCTCATGTGC CTTTTCATGT CAGGTGTGAG 4320
AGGAGGGACT CAAAGGTGGA GGTCATAGAG CTACAGGACG TGGAATGTGA GGAGAGGCCG 4380
TGGGGGAGCA GCTCCAACTG AGGGTAATTA AAATCTGAAG CAAAGAGGCC AAAGATTGGA 4440
AAGCCCCGCC CCCACCTCTT TCCAGAACTG CTTGAAGAGA ACTGCTTGGA ATTATGGGAA 4500
GGCAGTTCAT TGTTACTGTA ACTGATTGTA TTATTKKGTG AAATATTTCT ATAAATATTT 4560
AARAGGTGTA CACATGTAAT ATACATGGAA ATGCTGTACA GTCTATTTCC TGGGGCCTCT 4620

CCACTCCTGC CCCAGAGTGG GGAGACCACA GGGGCCCTTT CCCCTGTGTA CATTGGTCTC 4680

TGTGCCACAA CCAAGCTTAA CTTAGTTTTA AAAAAAATCT CCCAGCATAT GTCGCTGCTG 4740

CTTAAATATT GTATAATTTA CTTGTATAAT TCTATGCAAA TATTGCTTAT GTAATAGGAT 4800

TATTTGTAAA GGTTTCTGTT TAAAATATTT TAAATTTGCA TATCACAACC CTGTGGTAGG 4860

ATGAATTGTT ACTGTTAACT TTTGAACACG CTATGCGTGG TAATTGTTTA ACGAGCAGAC 4920

ATGAAGAAAA CAGGTTAATC CCAGTGGCTT CTCTAGGGGT AGTTGTATAT GGTTCGCATG 4980

GGTGGATGTG TGTGTGCATG TGACTTTCCA ATGTACTGTA TTGTGGTTTG TTGTTGTTGT 5040

TGCTGTTGTT GTTCATTTTG GTGTTTTTGG TTGCTTTGTA TGATCTTAGC TCTGGCCTAG 5100

GTGGGCTGGG AAGGTCCAGG TCTTTTTCTG TCGTGATGCT GGTGGAAAGG TGACCCCAAT 5160

CATCTGTCCT ATTCTCTGGG ACTATTC 5187

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1434 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met Ala Ser Ala Gly Asn Ala Ala Gly Ala Leu Gly Arg Gln Ala Gly
1 5 10 15

Gly Gly Arg Arg Arg Arg Thr Gly Gly Pro His Arg Ala Ala Pro Asp
20 25 30

Arg Asp Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe Ala Leu
35 40 45

Glu Gln Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp
50 55 60

Leu Arg Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile
65 70 75 80

Gln Lys Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly
85 90 95

Ala Phe Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu
100 105 110

Glu Leu Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr
115 120 125

Thr Arg Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met
130 135 140

Ile Gln Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala
145 150 155 160

Leu Leu Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val
165 170 175

Tyr Met Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser
180 185 190

Gly Glu Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr
195 200 205

Leu Tyr Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly
210 215 220

Ala Lys Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu
225 230 235 240

Arg Trp Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys
245 250 255

Ile Asn Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu
260 265 270

Val Gly His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro
275 280 285

Asp Cys Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp
290 295 300

Val Ala Leu Val Leu Asn Gly Gly Cys Gln Gly Leu Ser Arg Lys Tyr
305 310 315 320

Met His Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ala
325 330 335

Thr Gly Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu
340 345 350

Met Thr Pro Lys Gln Met Tyr Glu His Phe Arg Gly Tyr Asp Tyr Val
355 360 365

Ser His Ile Asn Trp Asn Glu Asp Arg Ala Ala Ala Ile Leu Glu Ala
370 375 380

Trp Gln Arg Thr Tyr Val Glu Val Val His Gln Ser Val Ala Pro Asn
385 390 395 400

Ser Thr Gln Lys Val Leu Pro Phe Thr Thr Thr Thr Leu Asp Asp Ile
405 410 415

Leu Lys Ser Phe Ser Asp Val Ser Val Ile Arg Val Ala Ser Gly Tyr
420 425 430

Leu Leu Met Leu Ala Tyr Ala Cys Leu Thr Met Leu Arg Trp Asp Cys

435 440 445

Ser Lys Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala
450 455 460

Leu Ser Val Ala Ala Gly Leu Gly Leu Cys Ser Leu Ile Gly Ile Ser
465 470 475 480

Phe Asn Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly Val
485 490 495

Gly Val Asp Asp Val Phe Leu Leu Ala His Ala Phe Ser Glu Thr Gly
500 505 510

Gln Asn Lys Arg Ile Pro Phe Glu Asp Arg Thr Gly Glu Cys Leu Lys
515 520 525

Arg Thr Gly Ala Ser Val Ala Leu Thr Ser Ile Ser Asn Val Thr Ala
530 535 540

Phe Phe Met Ala Ala Leu Ile Pro Ile Pro Ala Leu Arg Ala Phe Ser
545 550 555 560

Leu Gln Ala Ala Val Val Val Val Phe Asn Phe Ala Met Val Leu Leu
565 570 575

Ile Phe Pro Ala Ile Leu Ser Met Asp Leu Tyr Arg Arg Glu Asp Arg
580 585 590

Arg Leu Asp Ile Phe Cys Cys Phe Thr Ser Pro Cys Val Ser Arg Val
595 600 605

Ile Gln Val Glu Pro Gln Ala Tyr Thr Glu Pro His Ser Asn Thr Arg
610 615 620

Tyr Ser Pro Pro Pro Pro Tyr Thr Ser His Ser Phe Ala His Glu Thr
625 630 635 640

His Ile Thr Met Gln Ser Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro
645 650 655

His Thr His Val Tyr Tyr Thr Thr Ala Glu Pro Arg Ser Glu Ile Ser
660 665 670

Val Gln Pro Val Thr Val Thr Gln Asp Asn Leu Ser Cys Gln Ser Pro
675 680 685

Glu Ser Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser
690 695 700

Ser Leu His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser
705 710 715 720

Phe Ala Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys
725 730 735

Val Val Val Ile Leu Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr
740 745 750

Gly Thr Thr Arg Val Arg Asp Gly Leu Asp Leu Thr Asp Ile Val Pro
755 760 765

Arg Glu Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe
770 775 780

Ser Phe Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn
785 790 795 800

Ile Gln His Leu Leu Tyr Asp Leu His Lys Ser Phe Ser Asn Val Lys
805 810 815

Tyr Val Met Leu Glu Glu Asn Lys Gln Leu Pro Gln Met Trp Leu His
820 825 830

Tyr Phe Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp
835 840 845

Trp Glu Thr Gly Arg Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp
850 855 860

Asp Gly Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp
865 870 875 880

Lys Pro Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala
885 890 895

Asp Gly Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp
900 905 910

Val Ser Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg
915 920 925

Pro His Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu
930 935 940

Thr Arg Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe
945 950 955 960

Pro Phe Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala
965 970 975

Ile Glu Lys Val Arg Val Ile Cys Asn Asn Tyr Thr Ser Leu Gly Leu
980 985 990

Ser Ser Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile
995 1000 1005

Ser Leu Arg His Trp Leu Leu Leu Ser Ile Ser Val Val Leu Ala Cys
1010 1015 1020

Thr Phe Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly
1025 1030 1035 1040

Ile Ile Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met
1045 1050 1055

Met Gly Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu

1060 1065 1070

Ile Ala Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu
1075 1080 1085

Ala Phe Leu Thr Ala Ile Gly Asp Lys Asn His Arg Ala Met Leu Ala
1090 1095 1100

Leu Glu His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu
1105 1110 1115 1120

Leu Gly Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg
1125 1130 1135

Tyr Phe Phe Ala Val Leu Ala Ile Leu Thr Val Leu Gly Val Leu Asn
1140 1145 1150

Gly Leu Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Cys Pro
1155 1160 1165

Glu Val Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro
1170 1175 1180

Glu Pro Pro Pro Ser Val Val Arg Phe Ala Val Pro Pro Gly His Thr
1185 1190 1195 1200

Asn Asn Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr
1205 1210 1215

Val Ser Gly Ile Ser Glu Glu Leu Arg Gln Tyr Glu Ala Gln Gln Gly
1220 1225 1230

Ala Gly Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro
1235 1240 1245

Val Phe Ala Arg Ser Thr Val Val His Pro Asp Ser Arg His Gln Pro
1250 1255 1260

Pro Leu Thr Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Ser
1265 1270 1275 1280

Pro Gly Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly
1285 1290 1295

Leu Arg Pro Pro Pro Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser
1300 1305 1310

Thr Glu Gly His Ser Gly Pro Ser Asn Arg Asp Arg Ser Gly Pro Arg
1315 1320 1325

Gly Ala Arg Ser His Asn Pro Arg Asn Pro Thr Ser Thr Ala Met Gly
1330 1335 1340

Ser Ser Val Pro Ser Tyr Cys Gln Pro Ile Thr Thr Val Thr Ala Ser
1345 1350 1355 1360

Ala Ser Val Thr Val Ala Val His Pro Pro Pro Gly Pro Gly Arg Asn
1365 1370 1375

Pro Arg Gly Gly Pro Cys Pro Gly Tyr Glu Ser Tyr Pro Glu Thr Asp
1380 1385 1390

His Gly Val Phe Glu Asp Pro His Val Pro Phe His Val Arg Cys Glu
1395 1400 1405

Arg Arg Asp Ser Lys Val Glu Val Ile Glu Leu Gln Asp Val Glu Cys
1410 1415 1420

Glu Glu Arg Pro Trp Gly Ser Ser Ser Asn
1425 1430

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 11 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Leu Ile Val Gly Gly
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Pro Phe Phe Trp Glu Gln Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGACGAATTC AARGTNCAYC ARYTNTGG 28

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 26 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGACGAATTC CYTCCCARAA RCANTC 26

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGACGAATTC YTNGANTGYT TYTGGGA 27

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 31 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CATACCAGCC AAGCTTGTCN GGCCARTGCA T 31

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5288 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GAATTCCGGG GACCGCAAGG AGTGCCGCGG AAGCGCCCGA AGGACAGGCT CGCTCGGCGC 60

GCCGGCTCTC GCTCTTCCGC GAACTGGATG TGGGCAGCGG CGGCCGCAGA GACCTCGGGA 120

CCCCCGCGCA ATGTGGCAAT GGAAGGCGCA GGGTCTGACT CCCCGGCAGC GGCCGCGGCC 180

GCAGCGGCAG CAGCGCCCGC CGTGTGAGCA GCAGCAGCGG CTGGTCTGTC AACCGGAGCC 240

CGAGCCCGAG CAGCCTGCGG CCAGCAGCGT CCTCGCAAGC CGAGCGCCCA GGCGCGCCAG 300

GAGCCCGCAG CAGCGGCAGC AGCGCGCCGG GCCGCCCGGG AAGCCTCCGT CCCCGCGGCG 360

GCGGCGGCGG CGGCGGCGGC AACATGGCCT CGGCTGGTAA CGCCGCCGAG CCCCAGGACC 420

GCGGCGGCGG CGGCAGCGGC TGTATCGGTG CCCCGGGACG GCCGGCTGGA GGCGGGAGGC 480

GCAGACGGAC GGGGGGGCTG CGCCGTGCTG CCGCGCCGGA CCGGGACTAT CTGCACCGGC 540

CCAGCTACTG CGACGCCGCC TTCGCTCTGG AGCAGATTTC CAAGGGGAAG GCTACTGGCC 600

GGAAAGCGCC ACTGTGGCTG AGAGCGAAGT TTCAGAGACT CTTATTTAAA CTGGGTTGTT 660

ACATTCAAAA AAACTGCGGC AAGTTCTTGG TTGTGGGCCT CCTCATATTT GGGGCCTTCG 720

CGGTGGGATT AAAAGCAGCG AACCTCGAGA CCAACGTGGA GGAGCTGTGG GTGGAAGTTG 780

GAGGACGAGT AAGTCGTGAA TTAAATTATA CTCGCCAGAA GATTGGAGAA GAGGCTATGT 840

TTAATCCTCA ACTCATGATA CAGACCCCTA AAGAAGAAGG TGCTAATGTC CTGACCACAG 900

AAGCGCTCCT ACAACACCTG GACTCGGCAC TCCAGGCCAG CCGTGTCCAT GTATACATGT 960

ACAACAGGCA GTGGAAATTG GAACATTTGT GTTACAAATC AGGAGAGCTT ATCACAGAAA 1020

CAGGTTACAT GGATCAGATA ATAGAATATC TTTACCCTTG TTTGATTATT ACACCTTTGG 1080

ACTGCTTCTG GGAAGGGGCG AAATTACAGT CTGGGACAGC ATACCTCCTA GGTAAACCTC 1140

CTTTGCGGTG GACAAACTTC GACCCTTTGG AATTCCTGGA AGAGTTAAAG AAAATAAACT 1200

ATCAAGTGGA CAGCTGGGAG GAAATGCTGA ATAAGGCTGA GGTTGGTCAT GGTTACATGG 1260

ACCGCCCCTG CCTCAATCCG GCCGATCCAG ACTGCCCCGC CACAGCCCCC AACAAAAATT 1320

CAACCAAACC TCTTGATATG GCCCTTGTTT TGAATGGTGG ATGTCATGGC TTATCCAGAA 1380

AGTATATGCA CTGGCAGGAG GAGTTGATTG TGGGTGGCAC AGTCAAGAAC AGCACTGGAA 1440

AACTCGTCAG CGCCCATGCC CTGCAGACCA TGTTCCAGTT AATGACTCCC AAGCAAATGT 1500

ACGAGCACTT CAAGGGGTAC GAGTATGTCT CACACATCAA CTGGAACGAG GACAAAGCGG 1560

CAGCCATCCT GGAGGCCTGG CAGAGGACAT ATGTGGAGGT GGTTCATCAG AGTGTCGCAC 1620

AGAACTCCAC TCAAAAGGTG CTTTCCTTCA CCACCACGAC CCTGGACGAC ATCCTGAAAT 1680

CCTTCTCTGA CGTCAGTGTC ATCCGCGTGG CCAGCGGCTA CTTACTCATG CTCGCCTATG 1740

CCTGTCTAAC CATGCTGCGC TGGGACTGCT CCAAGTCCCA GGGTGCCGTG GGGCTGGCTG 1800

GCGTCCTGCT GGTTGCACTG TCAGTGGCTG CAGGACTGGG CCTGTGCTCA TTGATCGGAA 1860

TTTCCTTTAA CGCTGCAACA ACTCAGGTTT TGCCATTTCT CGCTCTTGGT GTTGGTGTGG 1920

ATGATGTTTT TCTTCTGGCC CACGCCTTCA GTGAAACAGG ACAGAATAAA AGAATCCCTT 1980

TTGAGGACAG GACCGGGGAG TGCCTGAAGC GCACAGGAGC CAGCGTGGCC CTCACGTCCA 2040

TCAGCAATGT CACAGCCTTC TTCATGGCCG CGTTAATCCC AATTCCCGCT CTGCGGGCGT 2100

TCTCCCTCCA GGCAGCGGTA GTAGTGGTGT TCAATTTTGC CATGGTTCTG CTCATTTTTC 2160

CTGCAATTCT CAGCATGGAT TTATATCGAC GCGAGGACAG GAGACTGGAT ATTTTCTGCT 2220

GTTTTACAAG CCCCTGCGTC AGCAGAGTGA TTCAGGTTGA ACCTCAGGCC TACACCGACA 2280

CACACGACAA TACCCGCTAC AGCCCCCCAC CTCCCTACAG CAGCCACAGC TTTGCCCATG 2340

AAACGCAGAT TACCATGCAG TCCACTGTCC AGCTCCGCAC GGAGTACGAC CCCCACACGC 2400

ACGTGTACTA CACCACCGCT GAGCCGCGCT CCGAGATCTC TGTGCAGCCC GTCACCGTGA 2460

CACAGGACAC CCTCAGCTGC CAGAGCCCAG AGAGCACCAG CTCCACAAGG GACCTGCTCT 2520
CCCAGTTCTC CGACTCCAGC CTCCACTGCC TCGAGCCCCC CTGTACGAAG TGGACACTCT 2580
CATCTTTTGC TGAGAAGCAC TATGCTCCTT TCCTCTTGAA ACCAAAAGCC AAGGTAGTGG 2640
TGATCTTCCT TTTTCTGGGC TTGCTGGGGG TCAGCCTTTA TGGCACCACC CGAGTGAGAG 2700
ACGGGCTGGA CCTTACGGAC ATTGTACCTC GGGAAACCAG AGAATATGAC TTTATTGCTG 2760
CACAATTCAA ATACTTTTCT TTCTACAACA TGTATATAGT CACCCAGAAA GCAGACTACC 2820
CGAATATCCA GCACTTACTT TACGACCTAC ACAGGAGTTT CAGTAACGTG AAGTATGTCA 2880
TGTTGGAAGA AAACAAACAG CTTCCCAAAA TGTGGCTGCA CTACTTCAGA GACTGGCTTC 2940
AGGGACTTCA GGATGCATTT GACAGTGACT GGGAAACCGG GAAAATCATG CCAAACAATT 3000
ACAAGAATGG ATCAGACGAT GGAGTCCTTG CCTACAAACT CCTGGTGCAA ACCGGCAGCC 3060
GCGATAAGCC CATCGACATC AGCCAGTTGA CTAAACAGCG TCTGGTGGAT GCAGATGGCA 3120
TCATTAATCC CAGCGCTTTC TACATCTACC TGACGGCTTG GGTCAGCAAC GACCCCGTCG 3180
CGTATGCTGC CTCCCAGGCC AACATCCGGC CACACCGACC AGAATGGGTC CACGACAAAG 3240
CCGACTACAT GCCTGAAACA AGGCTGAGAA TCCCGGCAGC AGAGCCCATC GAGTATGCCC 3300
AGTTCCCTTT CTACCTCAAC GGGTTGCGGG ACACCTCAGA CTTTGTGGAG GCAATTGAAA 3360
AAGTAAGGAC CATCTGCAGC AACTATACGA GCCTGGGGCT GTCCAGTTAC CCCAACGGCT 3420
ACCCCTTCCT CTTCTGGGAG CAGTACATCG GCCTCCGCCA CTGGCTGCTG CTGTTCATCA 3480
GCGTGGTGTT GGCCTGCACA TTCCTCGTGT GCGCTGTCTT CCTTCTGAAC CCCTGGACGG 3540
CCGGGATCAT TGTGATGGTC CTGGCGCTGA TGACGGTCGA GCTGTTCGGC ATGATGGGCC 3600
TCATCGGAAT CAAGCTCAGT GCCGTGCCCG TGGTCATCCT GATCGCTTCT GTTGGCATAG 3660
GAGTGGAGTT CACCGTTCAC GTTGCTTTGG CCTTTCTGAC GGCCATCGGC GACAAGAACC 3720
GCAGGGCTGT GCTTGCCCTG GAGCACATGT TTGCACCCGT CCTGGATGGC GCCGTGTCCA 3780
CTCTGCTGGG AGTGCTGATG CTGGCGGGAT CTGAGTTCGA CTTCATTGTC AGGTATTTCT 3840
TTGCTGTGCT GGCGATCCTC ACCATCCTCG GCGTTCTCAA TGGGCTGGTT TTGCTTCCCG 3900
TGCTTTTGTC TTTCTTTGGA CCATATCCTG AGGTGTCTCC AGCCAACGGC TTGAACCGCC 3960
TGCCCACACC CTCCCCTGAG CCACCCCCCA GCGTGGTCCG CTTCGCCATG CCGCCCGGCC 4020
ACACGCACAG CGGGTCTGAT TCCTCCGACT CGGAGTATAG TTCCCAGACG ACAGTGTCAG 4080
GCCTCAGCGA GGAGCTTCGG CACTACGAGG CCCAGCAGGG CGCGGGAGGC CCTGCCCACC 4140
AAGTGATCGT GGAAGCCACA GAAAACCCCG TCTTCGCCCA CTCCACTGTG GTCCATCCCG 4200

AATCCAGGCA TCACCCACCC TCGAACCCGA GACAGCAGCC CCACCTGGAC TCAGGGTCCC 4260

TGCCTCCCGG ACGGCAAGGC CAGCAGCCCC GCAGGGACCC CCCCAGAGAA GGCTTGTGGC 4320

CACCCCTCTA CAGACCGCGC AGAGACGCTT TTGAAATTTC TACTGAAGGG CATTCTGGCC 4380

CTAGCAATAG GGCCCGCTGG GGCCCTCGCG GGGCCCGTTC TCACAACCCT CGGAACCCAG 4440

CGTCCACTGC CATGGGCAGC TCCGTGCCCG GCTACTGCCA GCCCATCACC ACTGTGACGG 4500

CTTCTGCCTC CGTGACTGTC GCCGTGCACC CGCCGCCTGT CCCTGGGCCT GGGCGGAACC 4560

CCCGAGGGGG ACTCTGCCCA GGCTACCCTG AGACTGACCA CGGCCTGTTT GAGGACCCCC 4620

ACGTGCCTTT CCACGTCCGG TGTGAGAGGA GGGATTCGAA GGTGGAAGTC ATTGAGCTGC 4680

AGGACGTGGA ATGCGAGGAG AGGCCCCGGG GAAGCAGCTC CAACTGAGGG TGATTAAAAT 4740

CTGAAGCAAA GAGGCCAAAG ATTGGAAACC CCCCACCCCC ACCTCTTTCC AGAACTGCTT 4800

GAAGAGAACT GGTTGGAGTT ATGGAAAAGA TGCCCTGTGC CAGGACAGCA GTTCATTGTT 4860

ACTGTAACCG ATTGTATTAT TTTGTTAAAT ATTTCTATAA ATATTTAAGA GATGTACACA 4920

TGTGTAATAT AGGAAGGAAG GATGTAAAGT GGTATGATCT GGGGCTTCTC CACTCCTGCC 4980

CCAGAGTGTG GAGGCCACAG TGGGGCCTCT CCGTATTTGT GCATTGGGCT CCGTGCCACA 5040

ACCAAGCTTC ATTAGTCTTA AATTTCAGCA TATGTTGCTG CTGCTTAAAT ATTGTATAAT 5100

TTACTTGTAT AATTCTATGC AAATATTGCT TATGTAATAG GATTATTTTG TAAAGGTTTC 5160

TGTTTAAAAT ATTTTAAATT TGCATATCAC AACCCTGTGG TAGTATGAAA TGTTACTGTT 5220

AACTTTCAAA CACGCTATGC GTGATAATTT TTTTGTTTAA TGAGCAGATA TGAAGAAAGC 5280

CCGGAATT 5288

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1447 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Ala Ser Ala Gly Asn Ala Ala Glu Pro Gln Asp Arg Gly Gly Gly
1 5 10 15

Gly Ser Gly Cys Ile Gly Ala Pro Gly Arg Pro Ala Gly Gly Gly Arg
20 25 30

Arg Arg Arg Thr Gly Gly Leu Arg Arg Ala Ala Ala Pro Asp Arg Asp
35 40 45

Tyr Leu His Arg Pro Ser Tyr Cys Asp Ala Ala Phe Ala Leu Glu Gln
50 55 60

Ile Ser Lys Gly Lys Ala Thr Gly Arg Lys Ala Pro Leu Trp Leu Arg
65 70 75 80

Ala Lys Phe Gln Arg Leu Leu Phe Lys Leu Gly Cys Tyr Ile Gln Lys
85 90 95

Asn Cys Gly Lys Phe Leu Val Val Gly Leu Leu Ile Phe Gly Ala Phe
100 105 110

Ala Val Gly Leu Lys Ala Ala Asn Leu Glu Thr Asn Val Glu Glu Leu
115 120 125

Trp Val Glu Val Gly Gly Arg Val Ser Arg Glu Leu Asn Tyr Thr Arg
130 135 140

Gln Lys Ile Gly Glu Glu Ala Met Phe Asn Pro Gln Leu Met Ile Gln
145 150 155 160

Thr Pro Lys Glu Glu Gly Ala Asn Val Leu Thr Thr Glu Ala Leu Leu
165 170 175

Gln His Leu Asp Ser Ala Leu Gln Ala Ser Arg Val His Val Tyr Met
180 185 190

Tyr Asn Arg Gln Trp Lys Leu Glu His Leu Cys Tyr Lys Ser Gly Glu
195 200 205

Leu Ile Thr Glu Thr Gly Tyr Met Asp Gln Ile Ile Glu Tyr Leu Tyr
210 215 220

Pro Cys Leu Ile Ile Thr Pro Leu Asp Cys Phe Trp Glu Gly Ala Lys
225 230 235 240

Leu Gln Ser Gly Thr Ala Tyr Leu Leu Gly Lys Pro Pro Leu Arg Trp
245 250 255

Thr Asn Phe Asp Pro Leu Glu Phe Leu Glu Glu Leu Lys Lys Ile Asn
260 265 270

Tyr Gln Val Asp Ser Trp Glu Glu Met Leu Asn Lys Ala Glu Val Gly
275 280 285

His Gly Tyr Met Asp Arg Pro Cys Leu Asn Pro Ala Asp Pro Asp Cys
290 295 300

Pro Ala Thr Ala Pro Asn Lys Asn Ser Thr Lys Pro Leu Asp Met Ala
305 310 315 320

Leu Val Leu Asn Gly Gly Cys His Gly Leu Ser Arg Lys Tyr Met His
325 330 335

Trp Gln Glu Glu Leu Ile Val Gly Gly Thr Val Lys Asn Ser Thr Gly

340 345 350

Lys Leu Val Ser Ala His Ala Leu Gln Thr Met Phe Gln Leu Met Thr
355 360 365

Pro Lys Gln Met Tyr Glu His Phe Lys Gly Tyr Glu Tyr Val Ser His
370 375 380

Ile Asn Trp Asn Glu Asp Lys Ala Ala Ala Ile Leu Glu Ala Trp Gln
385 390 395 400

Arg Thr Tyr Val Glu Val Val His Gln Ser Val Ala Gln Asn Ser Thr
405 410 415

Gln Lys Val Leu Ser Phe Thr Thr Thr Thr Leu Asp Asp Ile Leu Lys
420 425 430

Ser Phe Ser Asp Val Ser Val Ile Arg Val Ala Ser Gly Tyr Leu Leu
435 440 445

Met Leu Ala Tyr Ala Cys Leu Thr Met Leu Arg Trp Asp Cys Ser Lys
450 455 460

Ser Gln Gly Ala Val Gly Leu Ala Gly Val Leu Leu Val Ala Leu Ser
465 470 475 480

Val Ala Ala Gly Leu Gly Leu Cys Ser Leu Ile Gly Ile Ser Phe Asn
485 490 495

Ala Ala Thr Thr Gln Val Leu Pro Phe Leu Ala Leu Gly Val Gly Val
500 505 510

Asp Asp Val Phe Leu Leu Ala His Ala Phe Ser Glu Thr Gly Gln Asn
515 520 525

Lys Arg Ile Pro Phe Glu Asp Arg Thr Gly Glu Cys Leu Lys Arg Thr
530 535 540

Gly Ala Ser Val Ala Leu Thr Ser Ile Ser Asn Val Thr Ala Phe Phe
545 550 555 560

Met Ala Ala Leu Ile Pro Ile Pro Ala Leu Arg Ala Phe Ser Leu Gln
565 570 575

Ala Ala Val Val Val Val Phe Asn Phe Ala Met Val Leu Leu Ile Phe
580 585 590

Pro Ala Ile Leu Ser Met Asp Leu Tyr Arg Arg Glu Asp Arg Arg Leu
595 600 605

Asp Ile Phe Cys Cys Phe Thr Ser Pro Cys Val Ser Arg Val Ile Gln
610 615 620

Val Glu Pro Gln Ala Tyr Thr Asp Thr His Asp Asn Thr Arg Tyr Ser
625 630 635 640

Pro Pro Pro Pro Tyr Ser Ser His Ser Phe Ala His Glu Thr Gln Ile
645 650 655

Thr Met Gln Ser Thr Val Gln Leu Arg Thr Glu Tyr Asp Pro His Thr
660 665 670

His Val Tyr Tyr Thr Thr Ala Glu Pro Arg Ser Glu Ile Ser Val Gln
675 680 685

Pro Val Thr Val Thr Gln Asp Thr Leu Ser Cys Gln Ser Pro Glu Ser
690 695 700

Thr Ser Ser Thr Arg Asp Leu Leu Ser Gln Phe Ser Asp Ser Ser Leu
705 710 715 720

His Cys Leu Glu Pro Pro Cys Thr Lys Trp Thr Leu Ser Ser Phe Ala
725 730 735

Glu Lys His Tyr Ala Pro Phe Leu Leu Lys Pro Lys Ala Lys Val Val
740 745 750

Val Ile Phe Leu Phe Leu Gly Leu Leu Gly Val Ser Leu Tyr Gly Thr
755 760 765

Thr Arg Val Arg Asp Gly Leu Asp Leu Thr Asp Ile Val Pro Arg Glu
770 775 780

Thr Arg Glu Tyr Asp Phe Ile Ala Ala Gln Phe Lys Tyr Phe Ser Phe
785 790 795 800

Tyr Asn Met Tyr Ile Val Thr Gln Lys Ala Asp Tyr Pro Asn Ile Gln
805 810 815

His Leu Leu Tyr Asp Leu His Arg Ser Phe Ser Asn Val Lys Tyr Val
820 825 830

Met Leu Glu Glu Asn Lys Gln Leu Pro Lys Met Trp Leu His Tyr Phe
835 840 845

Arg Asp Trp Leu Gln Gly Leu Gln Asp Ala Phe Asp Ser Asp Trp Glu
850 855 860

Thr Gly Lys Ile Met Pro Asn Asn Tyr Lys Asn Gly Ser Asp Asp Gly
865 870 875 880

Val Leu Ala Tyr Lys Leu Leu Val Gln Thr Gly Ser Arg Asp Lys Pro
885 890 895

Ile Asp Ile Ser Gln Leu Thr Lys Gln Arg Leu Val Asp Ala Asp Gly
900 905 910

Ile Ile Asn Pro Ser Ala Phe Tyr Ile Tyr Leu Thr Ala Trp Val Ser
915 920 925

Asn Asp Pro Val Ala Tyr Ala Ala Ser Gln Ala Asn Ile Arg Pro His
930 935 940

Arg Pro Glu Trp Val His Asp Lys Ala Asp Tyr Met Pro Glu Thr Arg
945 950 955 960

Leu Arg Ile Pro Ala Ala Glu Pro Ile Glu Tyr Ala Gln Phe Pro Phe

965 970 975

Tyr Leu Asn Gly Leu Arg Asp Thr Ser Asp Phe Val Glu Ala Ile Glu
980 985 990

Lys Val Arg Thr Ile Cys Ser Asn Tyr Thr Ser Leu Gly Leu Ser Ser
995 1000 1005

Tyr Pro Asn Gly Tyr Pro Phe Leu Phe Trp Glu Gln Tyr Ile Gly Leu
1010 1015 1020

Arg His Trp Leu Leu Leu Phe Ile Ser Val Val Leu Ala Cys Thr Phe
1025 1030 1035 1040

Leu Val Cys Ala Val Phe Leu Leu Asn Pro Trp Thr Ala Gly Ile Ile
1045 1050 1055

Val Met Val Leu Ala Leu Met Thr Val Glu Leu Phe Gly Met Met Gly
1060 1065 1070

Leu Ile Gly Ile Lys Leu Ser Ala Val Pro Val Val Ile Leu Ile Ala
1075 1080 1085

Ser Val Gly Ile Gly Val Glu Phe Thr Val His Val Ala Leu Ala Phe
1090 1095 1100

Leu Thr Ala Ile Gly Asp Lys Asn Arg Arg Ala Val Leu Ala Leu Glu
1105 1110 1115 1120

His Met Phe Ala Pro Val Leu Asp Gly Ala Val Ser Thr Leu Leu Gly
1125 1130 1135

Val Leu Met Leu Ala Gly Ser Glu Phe Asp Phe Ile Val Arg Tyr Phe
1140 1145 1150

Phe Ala Val Leu Ala Ile Leu Thr Ile Leu Gly Val Leu Asn Gly Leu
1155 1160 1165

Val Leu Leu Pro Val Leu Leu Ser Phe Phe Gly Pro Tyr Pro Glu Val
1170 1175 1180

Ser Pro Ala Asn Gly Leu Asn Arg Leu Pro Thr Pro Ser Pro Glu Pro
1185 1190 1195 1200

Pro Pro Ser Val Val Arg Phe Ala Met Pro Pro Gly His Thr His Ser
1205 1210 1215

Gly Ser Asp Ser Ser Asp Ser Glu Tyr Ser Ser Gln Thr Thr Val Ser
1220 1225 1230

Gly Leu Ser Glu Glu Leu Arg His Tyr Glu Ala Gln Gln Gly Ala Gly
1235 1240 1245

Gly Pro Ala His Gln Val Ile Val Glu Ala Thr Glu Asn Pro Val Phe
1250 1255 1260

Ala His Ser Thr Val Val His Pro Glu Ser Arg His His Pro Pro Ser
1265 1270 1275 1280

Asn Pro Arg Gln Gln Pro His Leu Asp Ser Gly Ser Leu Pro Pro Gly
1285 1290 1295

Arg Gln Gly Gln Gln Pro Arg Arg Asp Pro Pro Arg Glu Gly Leu Trp
1300 1305 1310

Pro Pro Leu Tyr Arg Pro Arg Arg Asp Ala Phe Glu Ile Ser Thr Glu
1315 1320 1325

Gly His Ser Gly Pro Ser Asn Arg Ala Arg Trp Gly Pro Arg Gly Ala
1330 1335 1340

Arg Ser His Asn Pro Arg Asn Pro Ala Ser Thr Ala Met Gly Ser Ser
1345 1350 1355 1360

Val Pro Gly Tyr Cys Gln Pro Ile Thr Thr Val Thr Ala Ser Ala Ser
1365 1370 1375

Val Thr Val Ala Val His Pro Pro Pro Val Pro Gly Pro Gly Arg Asn
1380 1385 1390

Pro Arg Gly Gly Leu Cys Pro Gly Tyr Pro Glu Thr Asp His Gly Leu
1395 1400 1405

Phe Glu Asp Pro His Val Pro Phe His Val Arg Cys Glu Arg Arg Asp
1410 1415 1420

Ser Lys Val Glu Val Ile Glu Leu Gln Asp Val Glu Cys Glu Glu Arg
1425 1430 1435 1440

Pro Arg Gly Ser Ser Ser Asn
1445

WHAT IS CLAIMED IS:

1. A DNA sequence other than present in a chromosome encoding a *patched* gene other than the *Drosophila patched* gene or fragment thereof of at least about 12bp different from the sequence of the *Drosophila patched* gene.

2. A DNA sequence according to Claim 1, wherein said *patched* gene is a mammalian gene.

3. A DNA sequence according to Claim 1 for human, mouse, mosquito, butterfly or beetle *patched* gene.

4. A DNA sequence according to Claim 3, wherein said DNA sequence is a human sequence.

5. A DNA sequence according to Claim 4, wherein said DNA sequence is a mouse sequence.

6. A DNA sequence according to Claim 1, wherein said DNA sequence is a fragment of at least about 18bp.

7. A DNA sequence according to Claim 1 joined to a DNA sequence comprising a restriction enzyme recognition sequence.

8. An expression cassette comprising a transcriptional initiation region functional in an expression host, a DNA sequence according to Claim 1 under the transcriptional regulation of said transcriptional initiation region, and a transcriptional termination region functional in said expression host.

9. An expression cassette according to Claim 8, wherein said transcriptional initiation region is heterologous to said DNA sequence according to Claim 1.

10. An expression cassette according to Claim 8, wherein said transcriptional initiation region is homologous to said DNA sequence according to Claim 1 and includes the enhancer region.

11. A cell comprising an expression cassette according to Claim 8 as part of an extrachromosomal element or integrated into the genome of a host cell as a result of introduction of said expression cassette into said host cell and the cellular progeny of said host cell.

12. A cell according to Claim 11, further comprising the *patched* protein in the cellular membrane of said cell.

13. A cell according to Claim 11, wherein said *patched* protein is a mouse *patched* protein.

14. A cell according to Claim 11, wherein said *patched* gene is a human *patched* protein.

15. A cell according to Claim 11, wherein said transcriptional initiation region is a *Drosophila patched* gene transcriptional initiation region comprising the promoter and enhancer joined to a heterologous gene.

16. A cell comprising an expression cassette comprising a transcriptional initiation region functional in an expression host, said transcriptional initiation region consisting of a 5' non-coding region regulating the transcription of *patched* protein comprising the promoter and enhancer, a marker gene, and a transcriptional termination region, as part of an extrachromosomal element or integrated into the genome of a host cell as a result of introduction of said expression cassette into said host, and the cellular progeny thereof.

17. A cell according to Claim 16, wherein said transcriptional initiation region is the *Drosophila* region.

18. A method for following embryonic development employing the *patched* protein in an embryo, said method comprising:

integrating an expression cassette comprising a transcriptional initiation region functional in embryonic host cells, said transcriptional initiation region consisting of a 5' non-coding region regulating the transcription of *patched* protein, a marker gene, and a transcriptional termination region, wherein said embryonic host cells are capable of developing into a fetus;

growing said embryonic host cells, whereby proliferation and differentiation occur; and

locating cells comprising expression of the *patched* protein by means of expression of said marker gene.

19. A method for producing *patched* protein, said method comprising:

growing a cell according to Claim 11, whereby said *patched* protein is expressed; and

isolating said *patched* protein free of other proteins.

20. A method for screening candidate compounds for binding affinity to the *patched* protein, said method comprising:

combining said candidate protein with a vertebrate or invertebrate cell comprising said *patched* protein in the membrane of said cell and an expression cassette comprising a transcriptional initiation region functional in said cell, a DNA sequence according to Claim 1 comprising the entire coding sequence under the transcriptional regulation of said transcriptional initiation region, and a transcriptional termination region functional in said cell, expressing said *patched* protein in said cell; and

assaying for the binding of said candidate compound to said *patched* protein.

21. A method for screening candidate compounds for agonist activity with the *patched* protein, said method comprising:

combining said candidate protein with a vertebrate or invertebrate cell comprising said *patched* protein in the membrane of said cell and an expression cassette comprising a transcriptional initiation region functional in an expression host, said transcriptional initiation region consisting of a 5' non-coding region regulating the transcription of *patched* protein, a marker gene, and a transcriptional termination region, as part of an extrachromosomal element or integrated into the genome of a host cell; and

assaying for the expression of said marker gene.

22. A monoclonal antibody binding specifically to a *patched* protein, other than the *Drosophila patched* protein.

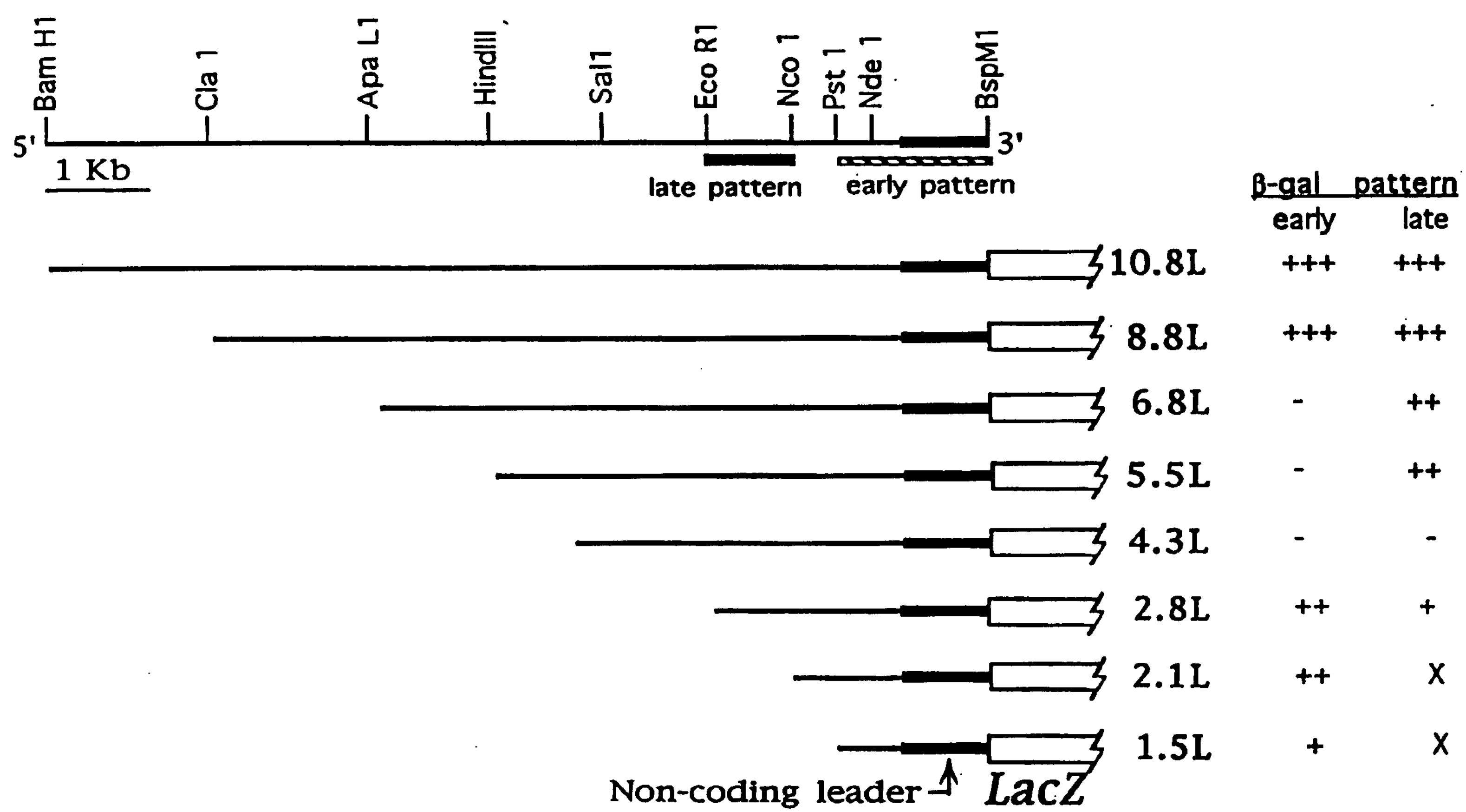
Bam H1
Cla 1
Apa L1
HindIII
Sal1
Eco R1
Nco 1
Pst 1
Nde 1
BspM1
5'
3'
1 Kb
late pattern
early pattern
β-gal pattern
early
late
10.8L +++ +++
8.8L +++ +++
6.8L - ++
5.5L - ++
4.3L - -
2.8L ++ +
2.1L ++ X
1.5L + X
Non-coding leader
LacZ

FIGURE 1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/13233

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C12N 5/00, 15/00; C07H 21/00
US CL : 536/23.1; 435/69.1, 172.3, 240.2, 320.1
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 536/23.1; 435/69.1, 172.3, 240.2, 320.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Please See Extra Sheet.

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Nature, Volume 341, issued 12 October 1989, Nakano et al., "A protein with several possible membrane-spanning domains encoded by the Drosophila segment polarity gene patched", pages 508-513, see the entire document.	1-10 and 18
Y	Cell, Volume 59, issued 17 November 1989, Hooper et al., "The Drosophila patched gene encodes a putative membrane protein required for segmental patterning", pages 751-765, see the entire document.	1-10 and 18
Y	Gene, Volume 112, issued 1992, Chavrier et al., "The complexity of the Rab and Rho GTP-binding protein subfamilies revealed by a PCR cloning approach", pages 261-264, see the entire document.	1-10

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search

19 JANUARY 1996

Date of mailing of the international search report

31 JAN 1996

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C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Biochemistry, Volume 31, No. 44, issued 1992, Ma et al., "Molecular cloning and characterization of rKlk10, a cDNA encoding T-kininogenase from rat submandibular gland and kidney', pages 10922-10928, see the experimental procedures on page 10923.	1-10
Y	Gene, Volume 74, issued 1988, Thummel et al., "Vectors for Drosophila P-element-mediated transformation and tissue culture transfection", pages 445-456, see the entire document.	8-10 and 18
Y	Developmental Genetics, Volume 12, issued 1991, Perrimon et al., "Generating lineage-specific markers to study Drosophila development", pages 238-252, see the entire document.	8-10 and 18

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/13233

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

Please See Extra Sheet.

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-10 AND 18

Remark on Protest
☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

B. FIELDS SEARCHED
Electronic data bases consulted (Name of data base and where practicable terms used):

APS, DIALOG
search terms: patched, gene, cloning, PCR, human, mammalian, mouse, mosquito, butterfly, beetle, DNA, drosophila, embryo, gal, galactosidase, develop, review, inventors' names

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION WAS LACKING
This ISA found multiple inventions as follows:

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be examined, the appropriate additional examination fees must be paid.

Group I, claims 1-10 and 18, drawn to a DNA sequence encoding a patched gene, an expression cassette, and a method for following embryonic development by integrating the expression cassette.

Group II, claims 11-17 and 19, drawn to a cell and a method for producing patched protein by growing the cell.

Group III, claim 20, drawn to a method for screening candidate compounds for binding affinity to the patched protein.

Group IV, claim 21, drawn to a method for screening candidate compounds for agonist activity with the patched protein.

Group V, claim 22, drawn to a monoclonal antibody specific for a patched protein.

The inventions listed as Groups I-V do not relate to a single inventive concept under PCT Rule 13.1, because, under PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons:

Groups I, II and V are not so linked as to form a single inventive concept because the DNA sequence of Group I, the cell of Group II and the monoclonal antibody of Group V are drawn to three different products.

Groups II and III are not so linked as to form a single inventive concept because they are drawn to materially different methods. The method of Group II involves growing a cell while the method of Group III involves combining a candidate compound with a cell and then assaying for binding.

Groups II and IV are not so linked as to form a single inventive concept because they are drawn to materially different methods. The method of Group II involves growing a cell while the method of Group IV involves combining a candidate compound with a cell and then assaying for expression of a marker gene.